GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 09:16:10 ; Search time 1464 Seconds
(without alignments)
2664.531 Million cell updates/sec

Title: US-09-806-701-15_COPY_991_1080
Perfect score: 90
Sequence: 1 gaacggatgatggctctgca.....gaacgctggacgacctagag 90

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
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2: gb_htg:*
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38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	90	100.0	771	6	AX053659	AX053659 Sequence
	2	90	100.0	1055	6	AR099307	AR099307 Sequence
	3	90	100.0	1659	6	AX024046	AX024046 Sequence
	4	90	100.0	2268	6	AR067807	AR067807 Sequence
	5	90	100.0	2268	6	AR084022	AR084022 Sequence
	6	90	100.0	2268	6	AR153351	AR153351 Sequence
	7	90	100.0	2268	6	AR153423	AR153423 Sequence
	8	90	100.0	2268	6	AR153426	AR153426 Sequence
	9	90	100.0	2268	6	AR253906	AR253906 Sequence
	10	90	100.0	2268	6	AX318491	AX318491 Sequence
	11	90	100.0	2268	6	BD062396	BD062396 IKK-alpha
	12	90	100.0	2268	6	BD062399	BD062399 IKK-beta
	13	90	100.0	2268	9	AF029684	AF029684 Homo sapi
	14	90	100.0	2271	6	AR162236	AR162236 Sequence
	15	90	100.0	2271	6	AR342527	AR342527 Sequence
	16	90	100.0	2271	6	BD009912	BD009912 Stimulus-
	17	90	100.0	2271	9	AF031416	AF031416 Homo sapi
	18	90	100.0	2783	9	AK091297	AK091297 Homo sapi
	19	90	100.0	2818	6	AX880268	AX880268 Sequence
	20	90	100.0	2818	6	BD158288	BD158288 Primer fo
	21	90	100.0	2818	9	AK023193	AK023193 Homo sapi
	22	90	100.0	2931	6	AR156758	AR156758 Sequence
	23	90	100.0	2931	6	BD082222	BD082222 I-kappa-B
	24	90	100.0	3018	6	AX024044	AX024044 Sequence
	25	90	100.0	3024	6	AX024040	AX024040 Sequence
	26	90	100.0	3058	9	AF080158	AF080158 Homo sapi
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	28	90	100.0	3966	6	AR099305	AR099305 Sequence
	29	86	95.6	2404	9	AK097828	AK097828 Homo sapi
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	33	77.2	85.8	3038	10	AF115282	AF115282 Rattus no
	34	74	82.2	2274	10	AF026524	AF026524 Mus muscu
	35	74	82.2	3572	10	BC037723	BC037723 Mus muscu
	36	74	82.2	4039	10	AF088910	AF088910 Mus muscu
c	37	73.2	81.3	274786	2	AC109661	AC109661 Rattus no
	38	70	77.8	225065	10	AC121835	AC121835 Mus muscu
	39	68.2	75.8	3490	4	BTA414556	AJ414556 Bos tauru
	40	36.2	40.2	3442	4	BTA414555	AJ414555 Bos tauru
	41	35.6	39.6	1874	6	AR258658	AR258658 Sequence
	42	35.6	39.6	2025	6	AR102061	AR102061 Sequence
	43	35.6	39.6	2056	10	BC018243	BC018243 Mus muscu
	44	35.6	39.6	3314	6	AR258657	AR258657 Sequence
	45	35.6	39.6	3466	6	AX306151	AX306151 Sequence

ALIGNMENTS

RESULT 1
AX053659
LOCUS AX053659 771 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 425 from Patent WO0073801.
ACCESSION AX053659
VERSION AX053659.1 GI:12227978
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Obata,Y.
TITLE Breast, gastric and prostate cancer associated antigens and uses therefor

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  JOURNAL   Patent: WO 0073801-A 425 07-DEC-2000;
            LUDWIG INSTITUTE FOR CANCER RESEARCH (US)
FEATURES             Location/Qualifiers
     source          1. .771
                     /organism="Homo sapiens"
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                     /db_xref="taxon:9606"
ORIGIN

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Db        112 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 171

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
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Db        172 AAGCAGGGGGGAACGCTGGACGACCTAGAG 201


RESULT 2
AR099307
LOCUS       AR099307                1055 bp    DNA     linear   PAT 14-FEB-2001
DEFINITION  Sequence 3 from patent US 6077701.
ACCESSION   AR099307
VERSION     AR099307.1  GI:12809073
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 1055)
  AUTHORS   Chu,K. and Pot,D.
  TITLE     Ikk.beta. regulates transcription factors
  JOURNAL   Patent: US 6077701-A 3 20-JUN-2000;
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ORIGIN

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Db        322 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 381

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
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Db        382 AAGCAGGGGGGAACGCTGGACGACCTAGAG 411


RESULT 3
AX024046
LOCUS       AX024046                1659 bp    DNA     linear   PAT 15-SEP-2000
DEFINITION  Sequence 15 from Patent WO0023091.
ACCESSION   AX024046
VERSION     AX024046.1  GI:10184361
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Scudder,K.M., Thastrup,O., Bjoern,S.P., Terry,B.R. and
            Arkhammar,P.O.
  TITLE     Specific therapeutic interventions obtained by interference with
            redistribution and/or targetting
  JOURNAL   Patent: WO 0023091-A 15 27-APR-2000;
            SCUDDER KURT MARSHALL (DK) ; BIOIMAGE A S (DK) ; THASTRUP OLE (DK)
            ; BJOERN SARA PETERSEN (DK) ; TERRY BERNARD ROBERT (DK) ; ARKHAMMAR
            PER O G (SE)
FEATURES             Location/Qualifiers
     source          1. .1659
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                     /mol_type="unassigned DNA"
                     /db_xref="taxon:32630"
     CDS             1. .1659
                     /note="unnamed protein product; fusion between Aequorea
                     victoria and human"
                     /codon_start=1
                     /transl_table=11
                     /protein_id="CAC08904.1"
                     /db_xref="GI:10184362"
                     /db_xref="REMTREMBL:CAC08904"
                     /translation="MVSKGEELFTGVVPILVELDGDVNGHKFSVSGEGEGDATYGKLT
                     LKFICTTGKLPVPWPTLVTTLTYGVQCFSRYPDHMKQHDFFKSAMPEGYVQERTIFFK
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                     MVLLEFVTAAGITLGMDELYKSGLRSRAQASTMMNLLRNNSCLSKMKNSMASMSQQLK
                     AKLDFFKTSIQIDLEKYSEQTEFGITSDKLLLAWREMEQAVELCGRENEVKLLVERMM
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ORIGIN

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Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
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Db       1051 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1080


RESULT 4
AR067807
LOCUS       AR067807                2268 bp    DNA     linear   PAT 29-SEP-1999
DEFINITION  Sequence 1 from patent US 5851812.
ACCESSION   AR067807
VERSION     AR067807.1  GI:5999029
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2268)
  AUTHORS   Goeddel,D.V. and Woronicz,J.
  TITLE     IKK-.beta. proteins, nucleic acids and methods
  JOURNAL   Patent: US 5851812-A 1 22-DEC-1998;
FEATURES             Location/Qualifiers
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Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
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Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 5
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AR084022
LOCUS       AR084022                2268 bp    DNA     linear   PAT 01-SEP-2000
DEFINITION  Sequence 1 from patent US 5977341.
ACCESSION   AR084022
VERSION     AR084022.1  GI:10010793
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2268)
  AUTHORS   Monia,B.P. and Cowsert,L.M.
  TITLE     Antisense modulation of inhibitor-kappa B kinase-beta expression
  JOURNAL   Patent: US 5977341-A 1 02-NOV-1999;
FEATURES             Location/Qualifiers
     source          1. .2268
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Qy         61 AAGCAGGGGGGGAACGCTGGACGACCTAGAG 90
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RESULT 6
AR153351
LOCUS       AR153351                2268 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6235492.
ACCESSION   AR153351
VERSION     AR153351.1  GI:15120883
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2268)
  AUTHORS   Rothe,M., Cao,Z. and Regnier,C.
  TITLE     IKK-.alpha. proteins, nucleic acids and methods
  JOURNAL   Patent: US 6235492-A 1 22-MAY-2001;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
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Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 7
AR153423
LOCUS       AR153423                2268 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6235512.
ACCESSION   AR153423
VERSION     AR153423.1  GI:15120955
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2268)
  AUTHORS   Rothe,M., Cao,Z. and Regnier,C.
  TITLE     IKK-.alpha. proteins, nucleic acids and methods
  JOURNAL   Patent: US 6235512-A 1 22-MAY-2001;
FEATURES             Location/Qualifiers
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ORIGIN

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Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
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Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
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Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 8
AR153426
LOCUS       AR153426                2268 bp    DNA     linear   PAT 08-AUG-2001
DEFINITION  Sequence 1 from patent US 6235513.
ACCESSION   AR153426
VERSION     AR153426.1  GI:15120958
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2268)
  AUTHORS   Rothe,M., Cao,Z. and Regnier,C.
  TITLE     IKK-.alpha. proteins, nucleic acids and methods
  JOURNAL   Patent: US 6235513-A 1 22-MAY-2001;
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RESULT 9
AR253906
LOCUS       AR253906                2268 bp    mRNA    linear   PAT 20-DEC-2002
DEFINITION  Sequence 1 from patent US 6479266.
ACCESSION   AR253906
VERSION     AR253906.1  GI:27302384
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2268)
  AUTHORS   Rothe,M., Cao,Z. and Regnier,C.
  TITLE     IKK-.alpha. proteins nucleic acids and methods
  JOURNAL   Patent: US 6479266-A 1 12-NOV-2002;
FEATURES             Location/Qualifiers
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Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
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RESULT 10
AX318491
LOCUS       AX318491                2268 bp    DNA     linear   PAT 14-DEC-2001
DEFINITION  Sequence 1 from Patent WO0183554.
ACCESSION   AX318491
VERSION     AX318491.1  GI:17900949
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   May,M.J., Ghosh,S., Findeis,M.A. and Phillips,K.
  TITLE     Anti-inflammatory compounds and uses thereof
  JOURNAL   Patent: WO 0183554-A 1 08-NOV-2001;
            Praecis Pharmaceuticals Incorporated (US) ; YALE UNIVERSITY (US)
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:32630"
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ORIGIN

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Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 11
BD062396
LOCUS       BD062396                2268 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  IKK-alpha proteins, nucleic acids and methods.
ACCESSION   BD062396
VERSION     BD062396.1  GI:22607999
KEYWORDS    JP 2001510346-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2268)
  AUTHORS   Rothe,M., Cao,Z. and Regnier,C.
  TITLE     IKK-alpha proteins, nucleic acids and methods
  JOURNAL   Patent: JP 2001510346-A 1 31-JUL-2001;
            TULARIK INC
COMMENT     PN   JP 2001510346-A/1
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            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
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Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
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Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 12
BD062399
LOCUS       BD062399                2268 bp    DNA     linear   PAT 27-AUG-2002
DEFINITION  IKK-beta  proteins, nucleic acids and methods.
ACCESSION   BD062399
VERSION     BD062399.1  GI:22608002
KEYWORDS    JP 2001510347-A/1.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2268)
  AUTHORS   Goeddel,D.V. and Woronicz,J.
  TITLE     IKK-beta proteins, nucleic acids and methods
  JOURNAL   Patent: JP 2001510347-A 1 31-JUL-2001;
            TULARIK INC
COMMENT     PN   JP 2001510347-A/1
            PD   31-JUL-2001
            PF   01-JUL-1998 JP 1999507373
            PR   01-JUL-1997 US    08/887114,10-JUL-1997 US    08/890853 PI
            DAVID V GOEDDEL,JOHN WORONICZ
            PC   C12N9/12,C12Q1/48
            CC   Strandedness: Double;
            CC   Topology: Linear;
            FH   Key             Location/Qualifiers.
FEATURES             Location/Qualifiers
     source          1. .2268
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

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  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
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Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 13
AF029684
```

```
LOCUS       AF029684                2268 bp    mRNA    linear   PRI 15-NOV-1997
DEFINITION  Homo sapiens IkB kinase-beta (IKK-beta) mRNA, partial cds.
ACCESSION   AF029684
VERSION     AF029684.1  GI:2599557
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2268)
  AUTHORS   Woronicz,J.D., Gao,X., Cao,Z., Rothe,M. and Goeddel,D.V.
  TITLE     IkappaB kinase-beta: NF-kappaB activation and complex formation
            with IkappaB kinase-alpha and NIK
  JOURNAL   Science 278 (5339), 866-869 (1997)
  MEDLINE   98008814
   PUBMED   9346485
REFERENCE   2  (bases 1 to 2268)
  AUTHORS   Woronicz,J.D., Gao,X., Cao,Z., Rothe,M. and Goeddel,D.V.
  TITLE     Direct Submission
  JOURNAL   Submitted (09-OCT-1997) Biology, Tularik, Inc., Two Corporate
            Drive, S. San Francisco, CA 94080, USA
FEATURES             Location/Qualifiers
     source          1. .2268
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="Jurkat"
                     /cell_type="T cell"
     gene            1. .>2268
                     /gene="IKK-beta"
     CDS             1. .>2268
                     /gene="IKK-beta"
                     /codon_start=1
                     /product="IkB kinase-beta"
                     /protein_id="AAC51860.1"
                     /db_xref="GI:2599558"
                     /translation="MSWSPSLTTQTCGAWEMKERLGTGGFGNVIRWHNQETGEQIAIK
                     QCRQELSPRNRERWCLEIQIMRRLTHPNVVAARDVPEGMQNLAPNDLPLLAMEYCQGG
                     DLRKYLNQFENCCGLREGAILTLLSDIASALRYLHENRIIHRDLKPENIVLQQGEQRL
                     IHKIIDLGYAKELDQGSLCTSFVGTLQYLAPELLEQQKYTVTVDYWSFGTLAFECITG
                     FRPFLPNWQPVQWHSKVRQKSEVDIVVSEDLNGTVKFSSSLPYPNNLNSVLAERLEKW
                     LQLMLMWHPRQRGTDPTYGPNGCFKALDDILNLKLVHILNMVTGTIHTYPVTEDESLQ
                     SLKARIQQDTGIPEEDQELLQEAGLALIPDKPATQCISDGKLNEGHTLDMDLVFLFDN
                     SKITYETQISPRPQPESVSCILQEPKRNLAFFQLRKVWGQVWHSIQTLKEDCNRLQQG
                     QRAAMMNLLRNNSCLSKMKNSMASMSQQLKAKLDFFKTSIQIDLEKYSEQTEFGITSD
                     KLLLAWREMEQAVELCGRENEVKLLVERMMALQTDIVDLQRSPMGRKQGGTLDDLEEQ
                     ARELYRRLREKPRDQRTEGDSQEMVRLLLQAIQSFEKKVRVIYTQLSKTVVCKQKALE
                     LLPKVEEVVSLMNEDEKTVVRLQEKRQKELWNLLKIACSKVRGPVSGSPDSMNASRLS
                     QPGQLMSQPSTASNSLPEPAKKSEELVAEAHNLCTLLENAIQDTVREQDQSFTALDWS
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ORIGIN

  Query Match             100.0%;  Score 90;  DB 9;  Length 2268;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-14;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 14
AR162236
LOCUS       AR162236                2271 bp    DNA     linear   PAT 17-OCT-2001
DEFINITION  Sequence 8 from patent US 6258579.
ACCESSION   AR162236
VERSION     AR162236.1  GI:16229366
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2271)
  AUTHORS   Mercurio,F., Zhu,H., Barbosa,M., Li,J.Wu. and Murray,B.W.
  TITLE     Stimulus-inducible protein kinase complex and methods of use
            therefor
  JOURNAL   Patent: US 6258579-A 8 10-JUL-2001;
FEATURES             Location/Qualifiers
     source          1. .2271
                     /organism="unknown"
                     /mol_type="unassigned DNA"
ORIGIN

  Query Match             100.0%;  Score 90;  DB 6;  Length 2271;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-14;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 15
AR342527
LOCUS       AR342527                2271 bp    DNA     linear   PAT 17-AUG-2003
DEFINITION  Sequence 8 from patent US 6576437.
ACCESSION   AR342527
VERSION     AR342527.1  GI:33737583
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2271)
  AUTHORS   Mercurio,F., Zhu,H., Barbosa,M., Li,J.W. and Murray,B.W.
  TITLE     Stimulus-inducible protein kinase complex and methods of use
            therefor
  JOURNAL   Patent: US 6576437-A 8 10-JUN-2003;
FEATURES             Location/Qualifiers
     source          1. .2271
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

  Query Match             100.0%;  Score 90;  DB 6;  Length 2271;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-14;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
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Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


Search completed: September 23, 2004, 20:20:32
Job time : 1467 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 08:42:00 ; Search time 330 Seconds
(without alignments)
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Title: US-09-806-701-15_COPY_991_1080
Perfect score: 90
Sequence: 1 gaacggatgatggctctgca.....gaacgctggacgacctagag 90

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002s:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	90	100.0	506	8	ACH37132	Ach37132 Human end
2	90	100.0	771	4	AAF22846	Aaf22846 Human pro
3	90	100.0	1055	2	AAX89677	Aax89677 C-termina
4	90	100.0	1558	4	AAH33389	Aah33389 Human col
5	90	100.0	1659	3	AAA14961	Aaa14961 DNA encod
6	90	100.0	2268	2	AAX08919	Aax08919 Human I k
7	90	100.0	2268	2	AAZ31590	Aaz31590 Human inh
8	90	100.0	2268	2	AAV84689	Aav84689 Human IKK
9	90	100.0	2268	2	AAX98271	Aax98271 cDNA enco
10	90	100.0	2268	2	AAX79304	Aax79304 Human IKK
11	90	100.0	2268	3	AAC81425	Aac81425 Human I-k
12	90	100.0	2268	6	ABA96316	Aba96316 Human IKK
13	90	100.0	2268	7	ABX11974	Abx11974 Human IKK
14	90	100.0	2268	8	ACD66625	Acd66625 Human inh
15	90	100.0	2271	2	AAV22842	Aav22842 DNA encod
16	90	100.0	2818	4	AAH16296	Aah16296 Human cDN
17	90	100.0	2931	2	AAV32970	Aav32970 Human I-k
18	90	100.0	2998	3	AAF21148	Aaf21148 Human low
19	90	100.0	3018	3	AAA14960	Aaa14960 DNA encod
20	90	100.0	3024	3	AAA14958	Aaa14958 DNA encod
21	90	100.0	3058	3	AAA35026	Aaa35026 Human ade
22	90	100.0	3058	7	ABZ96842	Abz96842 Human nuc
23	90	100.0	3965	2	AAX89675	Aax89675 Full leng
24	90	100.0	8631	3	AAA35028	Aaa35028 Human ade
25	90	100.0	8631	3	AAF21150	Aaf21150 Human low
26	90	100.0	8631	7	ABZ96844	Abz96844 Human nuc
27	81.6	90.7	400	7	ACD92547	Acd92547 Human col
28	77.2	85.8	3038	8	ACD66707	Acd66707 Rat inhib
29	74	82.2	554	9	ADD34950	Add34950 Mouse mit
30	74	82.2	2274	8	ACD66672	Acd66672 Mouse inh
31	35.6	39.6	1874	7	ABX94013	Abx94013 Mouse I k
32	35.6	39.6	1875	8	ADA26740	Ada26740 cDNA IKKa
33	35.6	39.6	2025	3	AAA08830	Aaa08830 Murine I
34	35.6	39.6	3314	7	ABX94012	Abx94012 Mouse I k
35	35.6	39.6	3314	8	ADA26739	Ada26739 cDNA IKKa
36	35.6	39.6	3466	6	ABI99798	Abi99798 Mouse isc
37	35.6	39.6	3466	7	ACC58547	Acc58547 Mouse IKK
38	34.6	38.4	2146	2	AAX08917	Aax08917 Human ser
39	34.6	38.4	2146	3	AAC81422	Aac81422 Human con
40	34.6	38.4	2146	7	ABX11976	Abx11976 Conserved
41	34.6	38.4	2238	2	AAX08918	Aax08918 Human IKK
42	34.6	38.4	2238	2	AAV84690	Aav84690 Human IKK
43	34.6	38.4	2238	2	AAX98272	Aax98272 cDNA enco
44	34.6	38.4	2238	2	AAX79305	Aax79305 Human IKK
45	34.6	38.4	2238	3	AAC81424	Aac81424 Human I-k

ALIGNMENTS

RESULT 1
ACH37132
ID ACH37132 standard; cDNA; 506 BP.
XX
AC ACH37132;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human endothelial cell cDNA #5265.
XX
KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX
OS Homo sapiens.
XX
PN US2003073623-A1.
XX
PD 17-APR-2003.
XX
PF 30-JUL-2001; 2001US-00918995.
XX
PR 30-JUL-2001; 2001US-00918995.
XX
PA (DRMA/) DRMANAC R T.
PA (LABA/) LABAT I.
PA (STAC/) STACHE-CRAIN B.
PA (DICK/) DICKSON M C.
PA (JONE/) JONES L W.
XX
PI Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX
DR WPI; 2003-615964/58.
XX
PT New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
PS Claim 1; SEQ ID NO 24344; 44pp; English.
XX
CC The invention relates to an isolated polynucleotide comprising any one of
CC 38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC determined by the technique of SBH (sequencing by hybridisation). Also
CC included is a purified polypeptide comprising a sequence corresponding to
CC a reading frame of the novel polynucleotide. The nucleic acid sequences
CC are useful in diagnostics as expressed sequence tags (EST) for

```
CC   identifying expressed genes or for physical mapping of the human genome,
CC   in forensics, in assessing biodiversities, or in identifying mutations
CC   responsible for genetic disorders and other traits. The nucleotide
CC   sequences are also useful as hybridisation probes, as oligomers for PCR,
CC   for chromosome and gene mapping, in the recombinant production of
CC   protein, or in generating antisense DNA or RNA. The purified polypeptide
CC   is useful for generating antibodies specific for it. The present sequence
CC   is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC   for this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from USPTO at
CC   seqdata.uspto.gov/sequence.html?DocID=20030073623
XX
SQ   Sequence 506 BP; 144 A; 96 C; 167 G; 95 T; 0 U; 4 Other;

  Query Match           100.0%;  Score 90;  DB 8;  Length 506;
  Best Local Similarity  100.0%;  Pred. No. 1.2e-19;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
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Db         64 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 123

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db        124 AAGCAGGGGGGAACGCTGGACGACCTAGAG 153


RESULT 2
AAF22846
ID   AAF22846 standard; cDNA; 771 BP.
XX
AC   AAF22846;
XX
DT   26-MAR-2001  (first entry)
XX
DE   Human prostate cancer associated antigen nucleotide sequence SEQ ID:425.
XX
KW   Human; breast cancer; gastric cancer; prostate cancer; diagnosis;
KW   cancer associated antigen; cytostatic; cancer vaccine; ss.
XX
OS   Homo sapiens.
XX
PN   WO200073801-A2.
XX
PD   07-DEC-2000.
XX
PF   26-MAY-2000; 2000WO-US014749.
XX
PR   28-MAY-1999;   99US-0136526P.
PR   10-SEP-1999;   99US-0153454P.
XX
PA   (LUDW-) LUDWIG INST CANCER RES.
XX
PI   Obata Y;
XX
DR   WPI; 2001-025274/03.
XX
PT   Nucleic acids encoding breast, gastric and prostate cancer associated
PT   antigen precursors, useful for diagnosing and treating a condition
PT   characterized by expression of an abnormal amount of a protein, e.g.
PT   cancer.
XX
PS   Claim 50; Page 413; 799pp; English.
XX
CC   AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
CC   represent nucleotide sequences encoding human breast, gastric and
CC   prostate cancer associated antigen precursors (CAAP) respectively.
CC   AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970
CC   represent human breast, gastric and prostate CAAP protein sequence
CC   respectively. CAAPs have cytostatic activity and can be used in the
CC   production of cancer vaccines. The human CAAP proteins, peptides, nucleic
CC   acids or anti-CAAP antibodies are useful for diagnosing and treating a
CC   condition characterised by expression of an abnormal amount of a protein,
CC   e.g. cancer
XX
SQ   Sequence 771 BP; 213 A; 176 C; 210 G; 157 T; 0 U; 15 Other;

  Query Match           100.0%;  Score 90;  DB 4;  Length 771;
  Best Local Similarity  100.0%;  Pred. No. 1.3e-19;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        112 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 171

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db        172 AAGCAGGGGGGAACGCTGGACGACCTAGAG 201


RESULT 3
AAX89677
ID   AAX89677 standard; DNA; 1055 BP.
XX
AC   AAX89677;
XX
DT   28-SEP-1999  (first entry)
XX
DE   C-terminal HLH domain of IKKbeta.
XX
KW   inflammatory disease; kinase; NFkappaB; transcription factor; IKKbeta;
KW   IKKB; phosphorylation; drug development; C-terminal; ss.
XX
OS   Homo sapiens.
XX
PN   WO9934000-A1.
XX
PD   08-JUL-1999.
XX
PF   30-DEC-1998;   98WO-US027917.
XX
PR   30-DEC-1997;   97US-0068954P.
PR   18-DEC-1998;   98US-00215131.
XX
PA   (CHIR ) CHIRON CORP.
XX
PI   Chu K,  Pot D;
XX
DR   WPI; 1999-430247/36.
XX
PT   New I-kappa-B kinase polynucleotides and polypeptides.
XX
PS   Claim 1; Page 40; 40pp; English.
XX
CC   Sequence AAX89675 represents the full length DNA sequence of IKKbeta,
CC   while sequence AAX89676 and AAX89677, encode for the N-terminal kinase
CC   domain and C-terminal HLH domain of IKKbeta respectively. The proteins
CC   may be alternatively spliced forms of IKKbeta. The IKK beta enzyme binds
CC   to and phosphorylates I-kappa-B protein. The IKKbeta polypeptides and
CC   fragments can be used to raise antibodies, which can then be used in
CC   immunochemical assays, to detect the presence of mutations in the
CC   IKKkappa gene which result in altered expression of the protein, to
CC   detect wild type IKKkappa in tissue samples. IKKkappa polynucleotides are
CC   a source of probes and primers, and can be used to produce recombinant
CC   protein. The polynucleotides are also a source of antisense sequences,
CC   which can be used to decrease expression of the IKKkappa gene. The
CC   protein can be used to screen for test compounds for use as inflammation
CC   inhibitors (claimed). IKK proteins are critical targets for anti-
CC   inflammatory drug development
XX
SQ   Sequence 1055 BP; 300 A; 248 C; 300 G; 207 T; 0 U; 0 Other;

  Query Match           100.0%;  Score 90;  DB 2;  Length 1055;
  Best Local Similarity  100.0%;  Pred. No. 1.4e-19;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
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Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
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Db        322 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 381

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db        382 AAGCAGGGGGGAACGCTGGACGACCTAGAG 411
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RESULT 4
AAH33389
ID AAH33389 standard; cDNA; 1558 BP.
XX
AC AAH33389;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen encoding cDNA SEQ ID NO:445.
XX
KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; chromosome 8; ss.
XX
OS Homo sapiens.
XX
PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PF 28-SEP-2000; 2000WO-US026524.
XX
PR 29-SEP-1999; 99US-0157137P.
PR 03-NOV-1999; 99US-0163280P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
DR WPI; 2001-235357/24.
DR P-PSDB; AAG73958.
XX
PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
PT useful for preventing, diagnosing and/or treating colorectal cancers.
XX
PS Claim 1; Page 2542; 9803pp; English.
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
CC proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene therapy
CC and vaccine production. N and P may be used in the prevention, diagnosis
CC and treatment of diseases associated with inappropriate P expression. For
CC example, N and P may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of P by expressing inactive proteins or to
CC supplement the patients own production of P. Additionally, N may be used
CC to produce the colon cancer-associated Ps, by inserting the nucleic acids
CC into a host cell and culturing the cell to express the proteins. N and P
CC can be used in the prevention, diagnosis and treatment of colorectal
CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
CC sequences used in the exemplification of the present invention. N.B.
CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
CC time of publication, meaning no sequences are present for SEQ ID NO:1027
CC to 1052, 7921 and 7922
XX
SQ Sequence 1558 BP; 445 A; 372 C; 427 G; 302 T; 0 U; 12 Other;

Query Match 100.0%; Score 90; DB 4; Length 1558;
Best Local Similarity 100.0%; Pred. No. 1.5e-19;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        817 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 876

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db        877 AAGCAGGGGGGAACGCTGGACGACCTAGAG 906
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RESULT 5
AAA14961
ID AAA14961 standard; DNA; 1659 BP.
XX
AC AAA14961;
XX
DT 21-AUG-2000 (first entry)
XX
DE DNA encoding a GFP-I-kappaB kinase-LZ domain fusion protein.
XX
KW I-kappaB kinase; cyclic nucleotide phosphodiesterase; cyclic AMP;
KW cyclic GMP; PDE3; PDE7; PDE8; PDE4 splice variant; PDE4D;
KW inflammatory disease; chronic inflammation; airway disease; asthma;
KW chronic bronchial hyper-reactivity; joint disorder; rheumatoid arthritis;
KW pelvospondylitis; bowel disease; ulcerative colitis; Crohn's disease;
KW autoimmune disease; diabetes mellitus type I; Hashimoto's thyroiditis;
KW systemic lupus erythromatosus; myasthenia gravis; Grave's disease;
KW immune thrombocytopenic purpura; acute respiratory distress syndrome;
KW septic shock; depression; PDE1; PDE2; PDE6; PDE9; PDE10; jet lag;
KW PDE5 splice variant; tension; erectile dysfunction; circadian rhythm;
KW green fluorescent protein; GFP; ss.
XX
OS Synthetic.
OS Homo sapiens.
OS Aequorea victoria.
XX
FH Key Location/Qualifiers
FT CDS 1. .1659
FT /*tag= a
XX
PN WO200023091-A2.
XX
PD 27-APR-2000.
XX
PF 15-OCT-1999; 99WO-DK000567.
XX
PR 15-OCT-1998; 98DK-00001321.
PR 15-OCT-1998; 98DK-00001322.
PR 15-OCT-1998; 98DK-00001323.
XX
PA (BIOI-) BIOIMAGE AS.
XX
PI Arkhammar POG, Terry BR, Scudder KM, Bjorn SP, Thastrup O;
XX
DR WPI; 2000-399281/34.
DR P-PSDB; AAY84883.
XX
PT Modulating the activity of I-kappaB kinases or cyclic nucleotide
PT phosphodiesterases for the treatment of inflammatory disorders,
PT autoimmune disorders (e.g. diabetes and Crohn's disease) and depression.
XX
PS Example 3; Page 125-127; 128pp; English.
XX
CC The specification describes a method for modulating the specific
CC effectiveness of I-kappaB kinases or cyclic nucleotide phosphodiesterases
CC which have the ability to cleave cyclic AMP and/or GMP. This involves
CC modulating the specific effectiveness of the cyclic nucleotide
CC phosphodiesterase or I-kappaB kinase by modulating the spatial
CC distribution within cells of the animal. If the cyclic nucleotide
CC phosphodiesterase used is a PDE3, PDE7, PDE8 or a splice variant of PDE4
CC (such as PDE4D), the method is used to treat inflammatory diseases such
CC as chronic inflammation (especially airway diseases such as asthma and
CC chronic bronchial hyper-reactivity of non-asthma etiology, joint
CC disorders such as rheumatoid arthritis and pelvospondylitis and bowel
CC diseases such as ulcerative colitis and Crohn's disease), autoimmune
CC diseases associated with inflammation (such as diabetes mellitus type I,
CC systemic lupus erythromatosus, myasthenia gravis, Hashimoto's

```
CC   thyroiditis, Grave's disease and immune thrombocytopenic purpura),
CC   disregulations of the immune system (such as acute respiratory distress
CC   syndrome (ARDS) and septic shock) and/or depression. Alternatively, if
CC   the cyclic nucleotide phosphodiesterase is PDE1, PDE2, PDE6, PDE9, PDE10
CC   or a splice variant of PDE5, the method is used to treat hypo- or
CC   hypertension, erectile dysfunction, circadian rhythm resetting or jet-
CC   lag. The present sequence encodes a fusion protein of green fluorescent
CC   protein (GFP) and I-kappaB kinase and the LZ domain, which is used in the
CC   course of the invention
XX
SQ   Sequence 1659 BP; 437 A; 461 C; 486 G; 275 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 90;  DB 3;  Length 1659;
  Best Local Similarity   100.0%;  Pred. No. 1.6e-19;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1050

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db       1051 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1080


RESULT 6
AAX08919
ID   AAX08919 standard; cDNA; 2268 BP.
XX
AC   AAX08919;
XX
DT   27-APR-1999  (first entry)
XX
DE   Human I kappa B kinase coding sequence.
XX
KW   I-kappa-B kinase; IKK-alpha; gene expression; modulation; suppression;
KW   activation; tumour necrosis factor; TNF; interleukin-1; IL-1;
KW   TNF receptor associated factor; TRAF; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2268
FT                   /*tag=  a
FT                   /label= I_kappa_B_kinase
XX
PN   WO9901541-A1.
XX
PD   14-JAN-1999.
XX
PF   01-JUL-1998;   98WO-US013782.
XX
PR   01-JUL-1997;   97US-00887115.
PR   10-JUL-1997;   97US-00890854.
XX
PA   (TULA-) TULARIK INC.
XX
PI   Rothe M,  Cao Z,  Regnier C;
XX
DR   WPI; 1999-106044/09.
DR   P-PSDB; AAW96158.
XX
PT   Newly isolated human kinase IkappaB Kinase (IKK--a) polypeptides - useful
PT   in screening for agents that modulate the interaction of an IKK
PT   polypeptide to a binding target and for modulating signal transduction
PT   involving IkappaB in a cell.
XX
PS   Disclosure; Page 20; 32pp; English.
XX
CC   I-kappa-B, deletion mutants of it retaining I-kappa-B kinase activity and
CC   I-kappa-B polypeptides (comprising a six residue domain of I-kappa-B
CC   containing one of Ser32 and Ser36, and a candidate agent) can be used to
CC   screen for agents that modulate the interaction of an IKK polypeptide to
CC   a binding target. The modulation of the kinase activity of IKK-alpha
CC   (AAW96157) forms a method for modulating signal transduction involving I-
CC   kappa-B in a cell. The IKK-alpha polypeptides are useful for generating
CC   oligonucleotide primers and probes for use in the isolation of natural
CC   IKK-alpha-encoding nucleic acids. The nucleic acids are useful as
CC   translatable transcripts, hybridization probes, polymerase chain reaction
CC   (PCR) probes and primers. Their diagnostic applications include IKK-alpha
CC   hybridization probes for identifying wild-type and mutant IKK-alpha
CC   alleles in clinical and laboratory samples. Therapeutic application
CC   includes the use of IKK-alpha nucleic acids for modulating cellular
CC   expression or intracellular concentration/availability of active IKK-
CC   alpha. Catalytically inactive IKK-alpha mutants suppress NF-kappa-B
CC   activation induced by tissue necrosis factor (TNF), interleukin-1 (IL-1)
CC   stimulation, TNF receptor-associated factor (TRAF) and NF-kappa-B-
CC   inducing kinase (NIK) oversuppression
XX
SQ   Sequence 2268 BP; 603 A; 569 C; 661 G; 435 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 90;  DB 2;  Length 2268;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-19;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 7
AAZ31590
ID   AAZ31590 standard; DNA; 2268 BP.
XX
AC   AAZ31590;
XX
DT   13-JAN-2000  (first entry)
XX
DE   Human inhibitor-kappa B kinase-beta coding sequence.
XX
KW   Inhibitor-kappa B kinase-beta; IKB-beta; human; T-cell leukaemia; asthma;
KW   inflammatory response; inflammatory disease; juvenile diabetes mellitus;
KW   Graves' disease; rheumatoid arthritis; allograft rejection; diagnosis;
KW   inflammatory bowel disease; multiple sclerosis; contact dermatitis;
KW   rhinitis; allergy; hyperproliferative disorder; tumour; therapy; ss.
XX
OS   Homo sapiens.
XX
PN   US5977341-A.
XX
PD   02-NOV-1999.
XX
PF   20-NOV-1998;   98US-00197008.
XX
PR   20-NOV-1998;   98US-00197008.
XX
PA   (ISIS-) ISIS PHARM INC.
XX
PI   Monia BP,  Cowsert LM;
XX
DR   WPI; 1999-619715/53.
DR   P-PSDB; AAY43247.
XX
PT   Antisense oligonucleotides inhibiting human Inhibitor-kappa B Kinase-
PT   beta, useful for treating conditions such as inflammation, asthma,
PT   diabetes, allograft rejection, allergies, hyperproliferative disorders or
PT   tumors.
XX
PS   Claim 1; Col 41-48; 32pp; English.
XX
CC   This sequence encodes the human inhibitor-kappa B kinase-beta. The
CC   invention relates to an antisense oligonucleotide (I) 8 to 30 nucleotides
```

```
CC   in length inhibiting the expression of human Inhibitor-kappa B kinase-
CC   beta (IKB-beta). (I) inhibits the expression of human IKB-beta which
CC   plays a role in the development of T-cell leukaemia and in the activation
CC   of inflammatory responses. (I) is therefore useful for treating
CC   inflammatory diseases or disorders with an inflammatory component such as
CC   asthma, juvenile diabetes mellitus, Graves' disease, rheumatoid
CC   arthritis, allograft rejection, inflammatory bowel disease, multiple
CC   sclerosis, contact dermatitis, rhinitis and various allergies, or
CC   hyperproliferative disorders such as leukaemias and other tumours. (I)
CC   may also be used for detection of the above disorders
XX
SQ   Sequence 2268 BP; 603 A; 569 C; 661 G; 435 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 90;  DB 2;  Length 2268;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-19;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 8
AAV84689
ID   AAV84689 standard; cDNA; 2268 BP.
XX
AC   AAV84689;
XX
DT   03-MAR-1999  (first entry)
XX
DE   Human IKK-beta polypeptide encoding cDNA.
XX
KW   IKK-beta; IkappaB kinase; inhibitor; NF-kappaB; nuclear factor-kappaB;
KW   nuclear translocation; NF-kappaB-inducing kinase; NIK; recombinant;
KW   human; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2268
FT                   /*tag=  a
FT                   /product= "IKK-beta polypeptide"
FT                   /note= "the stop codon is not indicated"
XX
PN   US5851812-A.
XX
PD   22-DEC-1998.
XX
PF   10-JUL-1997;   97US-00890853.
XX
PR   01-JUL-1997;   97US-00887114.
XX
PA   (TULA-) TULARIK INC.
XX
PI   Woronicz J,  Goeddel DV;
XX
DR   WPI; 1999-080407/07.
DR   P-PSDB; AAW86163.
XX
PT   DNA encoding IKK-beta polypeptides - useful for producing recombinant
PT   polypeptides.
XX
PS   Claim 3; Col 11-14; 13pp; English.
XX
CC   This cDNA encodes a IKK-beta (IkappaB kinase) polypeptide. The IkappaB
CC   (inhibitor of nuclear factor (NF)-kappaB nuclear translocation) kinase is
CC   a NF-kappaB-inducing kinase (NIK)-interacting protein. A host cell
CC   containing a recombinant nucleic acid encoding the IKK-beta polypeptide
CC   can be used for the recombinant production of the polypeptide
XX
SQ   Sequence 2268 BP; 603 A; 569 C; 661 G; 435 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 90;  DB 2;  Length 2268;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-19;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 9
AAX98271
ID   AAX98271 standard; cDNA; 2268 BP.
XX
AC   AAX98271;
XX
DT   20-MAR-2003  (revised)
DT   01-OCT-1999  (first entry)
XX
DE   cDNA encoding human kinase I-kappa-B kinase (IKK-beta).
XX
KW   Nuclear factor kappa-B inducing kinase; NIK; NIK-interacting protein;
KW   human; I-kappa-B kinase; IKK-beta; IKK-beta disorder; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2268
FT                   /*tag=  a
FT                   /note= "no termination codon given"
XX
PN   US5939302-A.
XX
PD   17-AUG-1999.
XX
PF   17-JUN-1998;   98US-00099124.
XX
PR   01-JUL-1997;   97US-00887114.
PR   10-JUL-1997;   97US-00890853.
XX
PA   (TULA-) TULARIK INC.
XX
PI   Woronicz J,  Goeddel DV;
XX
DR   WPI; 1999-468406/39.
DR   P-PSDB; AAY24051.
XX
PT   Polypeptides comprising a novel I-kappa-B Kinase useful as hybridization
PT   probes.
XX
PS   Claim 4; Col 11-14; 13pp; English.
XX
CC   The present sequence encodes a human I-kappa-B kinase (IKK-beta). The
CC   protein is a nuclear factor kappa-B inducing kinase (NIK) interacting
CC   protein. The IKK-beta nucleic acids, polypeptides, and/or antibodies may
CC   be useful as hybridization primers or probes, translatable transcripts,
CC   diagnostic probes (e.g. for identifying the presence of IKK-beta in a
CC   sample), to detect mutant IKK-beta alleles, in the diagnosis and therapy
CC   of IKK-beta disorders, and in the identification of compounds or agents
CC   that are able to modulate IKK-beta function. (Updated on 20-MAR-2003 to
CC   correct PF field.)
XX
SQ   Sequence 2268 BP; 603 A; 569 C; 661 G; 435 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 90;  DB 2;  Length 2268;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-19;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;
```

```
Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692
```

RESULT 10
AAX79304
ID AAX79304 standard; cDNA; 2268 BP.
XX
AC AAX79304;
XX
DT 31-AUG-1999 (first entry)
XX
DE Human IKK-beta coding sequence.
XX
KW Human; IKK-beta; I-Kappa B-Kinase; inhibitory protein; diagnosis; NF-kB;
KW Nuclear Factor Kappa B; interaction; binding target; ds.
XX
OS Homo sapiens.
XX
PN US5916760-A.
XX
PD 29-JUN-1999.
XX
PF 17-JUN-1998; 98US-00099125.
XX
PR 01-JUL-1997; 97US-00887114.
PR 10-JUL-1997; 97US-00890853.
XX
PA (TULA-) TULARIK INC.
XX
PI Goeddel DV, Woronicz J;
XX
DR WPI; 1999-384722/32.
DR P-PSDB; AAY14515.
XX
PT Screening for agents which modulate the interaction of IKK-beta
PT polypeptides and their binding targets.
XX
PS Claim 4; Col 11-14; 14pp; English.
XX
CC This sequence represents the coding region for human IKK-beta, a novel
CC IkB Kinase (I-Kappa B-Kinase, one of a family of inhibitory proteins
CC which interact with Nuclear Factor Kappa B (NF-kB)). The invention
CC relates to a method of screening for agents which modulate the
CC interaction of human IKK-beta polypeptides and their binding targets.
CC Agents which modulate the IKK-beta binding are useful in a variety of
CC diagnostic and therapeutic applications where the disease is associated
CC with improper utilization of a pathway involving IKK-beta proteins (e.g.
CC NF-kB activation and IKK-beta-dependent transcriptional activation)
XX
SQ Sequence 2268 BP; 603 A; 569 C; 661 G; 435 T; 0 U; 0 Other;

Query Match 100.0%; Score 90; DB 2; Length 2268;
Best Local Similarity 100.0%; Pred. No. 1.7e-19;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692
```

RESULT 11
AAC81425
ID AAC81425 standard; cDNA; 2268 BP.
XX
AC AAC81425;
XX
DT 23-FEB-2001 (first entry)
XX
DE Human I-kappa-B kinase beta-subunit (IKK-beta) cDNA.
XX
KW Human; I-kappa-B kinase; IKK; antisense therapy; gene therapy;
KW cytokine expression inhibition; NF-kappa-B activation inhibition;
KW nuclear factor-kappa-B; rheumatoid arthritis; immune disorder; cancer;
KW IKK-beta; beta-subunit; ss.
XX
OS Homo sapiens.
XX
PN JP2000253884-A.
XX
PD 19-SEP-2000.
XX
PF 10-MAR-1999; 99JP-00063291.
XX
PR 10-MAR-1999; 99JP-00063291.
XX
PA (TOAG) TOA GOSEI CHEM IND LTD.
XX
DR WPI; 2000-658813/64.
XX
PT Antisense nucleic acid compound complementary to the subunit of IkappaB,
PT used to treat rheumatic arthritis, immune diseases and cancer.
XX
PS Claim 3; Page 13-14; 20pp; Japanese.
XX
CC The invention relates to an antisense oligonucelotide targetted to a gene
CC encoding a subunit of I-kappa-B kinase (IKK) which inhibits its
CC expression, and thereby inhibits expression of a cytokine such as IL-6
CC (interleukin-6). I-kappa-B kinase activates NF-kappa-B (nuclear factor-
CC kappa-B) which acts a transcriptional regulator of cytokine genes. The
CC antisense oligonucleotide can be used in gene therapy to treat rheumatoid
CC arthritis, immune disorders and cancers. Sequences AAC81422-C81426 are
CC cDNAs derived from genes whose expression may be inhibited using an
CC antisense oligonucleotide of the invention. The present sequence
CC represents a human IKK-beta subunit cDNA
XX
SQ Sequence 2268 BP; 603 A; 569 C; 661 G; 435 T; 0 U; 0 Other;

Query Match 100.0%; Score 90; DB 3; Length 2268;
Best Local Similarity 100.0%; Pred. No. 1.7e-19;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692
```

RESULT 12
ABA96316
ID ABA96316 standard; DNA; 2268 BP.
XX
AC ABA96316;
XX
DT 20-MAR-2002 (first entry)
XX
DE Human IKKbeta encoding polynucleotide GenBank No AR067807.
XX
KW Antiinflammatory; antiasthmatic; cytostatic; antipsoriatic; nootropic;
KW antirheumatic; antiarthritic; osteopathic; antibacterial; virucide;
KW immunosuppressive; dermatological; neuroprotective; antiatherosclerotic;
KW antiallergic; membrane translocation domain; NEMO binding domain; human;
KW cytokine; NFkappaB; IkappaB kinase beta; IKKbeta; cancer; psoriasis;

```
KW   rheumatoid arthritis; osteoarthritis; inflammatory bowel disease;
KW   autoimmune disorder; multiple sclerosis; transplant rejection;
KW   osteoporosis; Alzheimer's disease; atherosclerosis; viral infection;
KW   ataxia telangiectasia; allergy; anaphylaxis; eczema; arthritis; gene; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             2203. .2235
FT                   /*tag=  a
FT                   /product= "IKKbeta peptide"
XX
PN   WO200183554-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US014346.
XX
PR   02-MAY-2000; 2000US-0201261P.
PR   22-AUG-2000; 2000US-00643260.
XX
PA   (PRAE-) PRAECIS PHARM INC.
PA   (UYYA ) UNIV YALE.
XX
PI   May MJ,  Ghosh S,  Findeis MA,  Phillips K;
XX
DR   WPI; 2002-121889/16.
DR   P-PSDB; AAM48506.
XX
PT   Novel antiinflammatory compound comprising membrane translocation domain
PT   fused to NEMO binding sequence, useful for blocking nuclear factor kappaB
PT   activation, and for treating asthma, lung inflammation, psoriasis.
XX
PS   Disclosure; Page; 88pp; English.
XX
CC   The invention relates to an antiinflammatory compound (especially
CC   AAM48628-AAM48645), comprising a membrane translocation domain (AAM48620-
CC   AMM48627 or AAM48646-AAM48651) which comprises from 6-15 amino acid
CC   residues, fused to a NEMO binding sequence (AAM48525-AAM48619). The
CC   antiinflammatory compounds have antiasthmatic, cytostatic, antipsoriatic,
CC   antirheumatic, antiarthritic, osteopathic, antibacterial,
CC   immunosuppressive, dermatological, neuroprotective, nootropic,
CC   antiatherosclerotic, virucide and antiallergic activity. The compounds
CC   act as selective inhibitors of cytokine-mediated NFkappaB activation by
CC   blocking interaction of IkappaB kinase beta (IKKbeta) at the NEMO binding
CC   domain that results in inhibition of IKKbeta kinase activation and
CC   subsequent decreased phosphorylation of IkappaB. The compounds are useful
CC   for treating inflammatory disorders, e.g. asthma, lung inflammation or
CC   cancer, psoriasis, rheumatoid arthritis, osteoarthritis, inflammatory
CC   bowel disease, sepsis, vasculitis, bursitis; autoimmune diseases such as
CC   lupus, polymyalgia, scleroderma, granulomatosis, multiple sclerosis;
CC   transplant rejection; osteoporosis; Alzheimer's disease; atherosclerosis;
CC   viral infections; and ataxia telangiectasia. The compounds are also
CC   useful for treating pro-inflammatory responses such as allergies,
CC   urticaria, anaphylaxis, drug or food sensitivity, eczema, dermatitis,
CC   sunburn, aging and arthritis. Note: The present sequence is not given in
CC   the printed specification but is that of human IKKbeta encoding
CC   polynucleotide derived from the sequence given at GenBank Number AR067807
XX
SQ   Sequence 2268 BP; 603 A; 569 C; 661 G; 435 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 90;  DB 6;  Length 2268;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-19;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692
```

```
RESULT 13
ABX11974
ID   ABX11974 standard; cDNA; 2268 BP.
XX
AC   ABX11974;
XX
DT   08-MAY-2003  (first entry)
XX
DE   Human IKK-alpha related cDNA.
XX
KW   Human; gene; ss; inhibitor of nuclear factor kappa-B kinase alpha;
KW   IKK-alpha; conserved helix-loop-helix ubiquitous kinase; CHUK; IKK-alpha;
KW   nuclear factor kappa B; NF-kappaB; cell regulation; IKK; phosphorylation;
KW   IkappaB; signal transduction disorder; genetic defect;
KW   autoimmune disease; neuroprotective; immunostimulant.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2268
FT                   /*tag=  a
FT                   /product= "IKK-alpha related polypeptide"
XX
PN   US6479266-B1.
XX
PD   12-NOV-2002.
XX
PF   02-JUL-1998;   98US-00109986.
XX
PR   01-JUL-1997;   97US-00887115.
PR   10-JUL-1997;   97US-00890854.
XX
PA   (TULA-) TULARIK INC.
XX
PI   Rothe M,  Cao Z,  Regnier C;
XX
DR   WPI; 2003-298112/29.
DR   P-PSDB; ABG75804.
XX
PT   New isolated IKK polypeptide involved in transcription factor activation,
PT   useful for diagnosing and treating disorders with aberrant activity of
PT   the IKK polypeptide, such as signal transduction disorders and genetic
PT   defects.
XX
PS   Disclosure; Col 13-16; 15pp; English.
XX
CC   The invention discloses methods and compositions relating to isolated
CC   inhibitor of nuclear factor kappa-B kinase alpha (IKK-alpha), also known
CC   as the conserved helix-loop-helix ubiquitous kinase (CHUK), polypeptides.
CC   IKK-alpha polypeptides regulate nuclear factor kappa B (NF-kappaB)
CC   activation and hence regulate cell function. Also disclosed are methods
CC   for screening for an agent which modulates the interaction of an IKK
CC   polypeptide to a binding target and for screening for an agent which
CC   modulates the ability of an IKK polypeptide to specifically phosphorylate
CC   an IkappaB polypeptide. The methods and compositions of the present
CC   invention are useful for the diagnosis and treatment of disorders
CC   associated with the aberrant activity of the IKK polypeptide, such as
CC   signal transduction disorders, genetic defects and autoimmune diseases.
CC   The sequence presented is the human IKK-alpha related cDNA
XX
SQ   Sequence 2268 BP; 603 A; 569 C; 661 G; 435 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 90;  DB 7;  Length 2268;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-19;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
```

```
Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 14
ACD66625
ID   ACD66625 standard; cDNA; 2268 BP.
XX
AC   ACD66625;
XX
DT   16-SEP-2003  (first entry)
XX
DE   Human inhibitor-kappa B kinase-beta DNA sequence.
XX
KW   Human; inhibitor-kappa B kinase-beta; anorectic; antidiabetic;
KW   antiinflammatory; cytostatic; gene therapy; antisense compound; obesity;
KW   diabetes type II; inflammatory disorder; cancer; leukaemia; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2003050270-A1.
XX
PD   13-MAR-2003.
XX
PF   24-MAY-2002; 2002US-00156610.
XX
PR   20-NOV-1998;   98US-00197008.
PR   28-JUL-1999;   99WO-US016959.
PR   30-AUG-2001; 2001US-00856246.
XX
PA   (MONI/) MONIA B P.
PA   (COWS/) COWSERT L M.
PA   (KOLL/) KOLLER E.
XX
PI   Monia BP,  Cowsert LM,  Koller E;
XX
DR   WPI; 2003-512357/48.
DR   P-PSDB; ABO32508.
XX
PT   New antisense compound, useful for preparing a composition for treating
PT   obesity, diabetes type II, inflammatory disorder or cancer e.g.,
PT   leukemia.
XX
PS   Example 13; Page 29-31; 49pp; English.
XX
CC   The invention describes a new antisense compound, which is 8-30
CC   nucleobases in length targeted to a nucleic acid molecule encoding
CC   Inhibitor-kappa B Kinase-beta that specifically hybridises with and
CC   inhibits the expression of Inhibitor-kappa B Kinase-beta. The compound is
CC   useful for preparing a composition for treating obesity, diabetes type
CC   II, inflammatory disorder or cancer e.g., leukaemia. This sequence
CC   represents human inhibitor-kappa B kinase-beta DNA
XX
SQ   Sequence 2268 BP; 603 A; 569 C; 661 G; 435 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 90;  DB 8;  Length 2268;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-19;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 15
AAV22842
ID   AAV22842 standard; DNA; 2271 BP.
XX
AC   AAV22842;
XX
DT   24-JUL-1998  (first entry)
XX
DE   DNA encoding inhibitory subunit I-kappa-B signalsome kinase 2.
XX
KW   Inhibitory subunit; I-kappa-B-beta; nuclear factor kappa-B;
KW   NF-kappa-B/Rel dimer; inhibitory activity; phosphorylation;
KW   stimulus-inducible I-kappa-B kinase; IKK; signalsome; I-kappa-B-alpha;
KW   identification; stimulate; signal transduction; the NF-kappa-B cascade;
KW   therapeutic composition; inflammatory; neurodegenerative; disease;
KW   autoimmune disease; cancer; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .2271
FT                   /*tag=  a
XX
PN   WO9808955-A1.
XX
PD   05-MAR-1998.
XX
PF   26-AUG-1997;   97WO-US015003.
XX
PR   26-AUG-1996;   96US-00697393.
PR   13-AUG-1997;   97US-00910820.
XX
PA   (SIGN-) SIGNAL PHARM INC.
XX
PI   Mercurio F,  Zhu H,  Barbosa M,  Li G,  Murray BW;
XX
DR   WPI; 1998-179440/16.
DR   P-PSDB; AAW56328.
XX
PT   New isolated stimulus-inducible I-kappa-B kinase signalsome - useful for
PT   developing products for treating, e.g. inflammatory neuro-degenerative
PT   and auto-immune diseases.
XX
PS   Disclosure; Page 58-60; 115pp; English.
XX
CC   The present sequence encodes an inhibitory subunit I-kappa-B kinase (IKK)
CC   2. IKK kinases, when incorporated into an IKK signalsome, are capable of
CC   phosphorylating inhibitory subunit I-kappa-B-alpha, at serine residues 32
CC   and 36. I-kappa-B-alpha retains nuclear factor (NF) kappa-B in the
CC   cytoplasm. I-kappa-B proteins contain 5-7 ankryin-like repeats which are
CC   required for association with the NF-kappa-B/Rel dimer and for inhibitory
CC   activity. A stimulus-inducible IKK "signalsome" is described that is
CC   capable of specifically phosphorylating I-kappa-B-alpha at residues S32
CC   and S36, without the addition of exogenous cofactors. The proteins of the
CC   invention can be used to identify agents that inhibit or stimulate signal
CC   transduction via the NF-kappa-B cascade. Therapeutic compositions
CC   comprising such agents may be used for treating a patient afflicted with
CC   a disorder associated with the activation of an IKK signalsome. The
CC   agents may be used to treat, e.g. inflammatory, neurodegenerative
CC   diseases and autoimmune diseases, cancer and viral infections. The
CC   antibodies may be used in a kit for detecting IKK signalsome activity in
CC   a sample
XX
SQ   Sequence 2271 BP; 604 A; 569 C; 661 G; 437 T; 0 U; 0 Other;

  Query Match             100.0%;  Score 90;  DB 2;  Length 2271;
  Best Local Similarity   100.0%;  Pred. No. 1.7e-19;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


Search completed: September 23, 2004, 19:55:55
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Job time : 332 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 14:33:31 ; Search time 2490 Seconds
(without alignments)
1079.356 Million cell updates/sec

Title: US-09-806-701-15_COPY_991_1080
Perfect score: 90
Sequence: 1 gaacggatgatggctctgca.....gaacgctggacgacctagag 90

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estmu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inv:*
19: em_gss_pln:*
20: em_gss_vrt:*
21: em_gss_fun:*
22: em_gss_mam:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rod:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*
29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	90	100.0	588	12	BG336659	BG336659 602405777
	2	90	100.0	589	12	BG107446	BG107446 602277558
	3	90	100.0	727	10	BE384533	BE384533 601277926
	4	90	100.0	745	12	BI084392	BI084392 602869515
	5	90	100.0	868	14	CD251031	CD251031 AGENCOURT
	6	90	100.0	944	13	BU857051	BU857051 AGENCOURT
	7	90	100.0	974	13	BQ669894	BQ669894 AGENCOURT
c	8	90	100.0	1201	9	AL542182	AL542182 AL542182
	9	88.4	98.2	878	13	BQ877352	BQ877352 AGENCOURT
c	10	86.8	96.4	557	10	BF590924	BF590924 7h46b08.x
	11	86	95.6	402	10	BE077902	BE077902 CM1-BT061
c	12	86	95.6	501	28	AQ827088	AQ827088 HS_5291_B
	13	86	95.6	864	14	CD299893	CD299893 AGENCOURT
	14	81.6	90.7	400	9	AI906358	AI906358 RC-BT108-
	15	79	87.8	401	10	AW997999	AW997999 RC1-BN005
c	16	78	86.7	736	14	CA429223	CA429223 UI-H-FH1-
	17	78	86.7	789	10	BE734952	BE734952 601571189
c	18	77.2	85.8	558	12	BI296436	BI296436 UI-R-CV2-
c	19	77.2	85.8	558	12	BI296613	BI296613 UI-R-CV2-
c	20	77.2	85.8	565	12	BI291377	BI291377 UI-R-CV2-
	21	77.2	85.8	714	14	CF113406	CF113406 Shultzomi
	22	76.4	84.9	946	13	BU558245	BU558245 AGENCOURT
	23	74	82.2	575	12	BG087220	BG087220 H3136H12-
	24	74	82.2	738	14	CF537632	CF537632 UI-M-GI0-
	25	74	82.2	741	10	BE310997	BE310997 601088571
	26	74	82.2	765	14	CD805176	CD805176 UI-M-GW0-
	27	74	82.2	943	13	BU511732	BU511732 AGENCOURT
	28	74	82.2	2193	11	BC004772	BC004772 Mus muscu
c	29	71	78.9	302	10	BF916026	BF916026 IL3-UT011
	30	69.8	77.6	465	10	AW656805	AW656805 109254 MA
	31	69.6	77.3	559	9	AA128064	AA128064 zl14c08.r
	32	69.2	76.9	732	13	BY764258	BY764258 BY764258
	33	68.2	75.8	390	12	BI976355	BI976355 485204 MA
	34	68.2	75.8	506	10	BF602600	BF602600 267870 MA
c	35	68	75.6	393	9	AI906367	AI906367 RC-BT108-
c	36	67.4	74.9	300	10	BF915824	BF915824 IL3-UT011
	37	66.2	73.6	718	10	BE687229	BE687229 uv94f03.y
	38	62.4	69.3	949	12	BG476715	BG476715 602524624
	39	62	68.9	342	10	BF834440	BF834440 CM2-HT096
	40	55.4	61.6	703	13	BU475878	BU475878 603470516
	41	54.6	60.7	622	12	BM489568	BM489568 pgm2n.pk0
	42	54.6	60.7	690	13	BU372250	BU372250 603808982
	43	54.6	60.7	780	13	BU373892	BU373892 603811752
	44	47.8	53.1	958	14	CA981256	CA981256 AGENCOURT
	45	43	47.8	616	10	AW955375	AW955375 EST367445

ALIGNMENTS

RESULT 1
BG336659
LOCUS BG336659 588 bp mRNA linear EST 27-FEB-2001
DEFINITION 602405777F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4543218 5', mRNA sequence.
ACCESSION BG336659
VERSION BG336659.1 GI:13143097
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 588)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1224 row: j column: 19
High quality sequence stop: 588.

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FEATURES             Location/Qualifiers
     source          1. .588
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4543218"
                     /tissue_type="choriocarcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_21"
                     /note="Organ: placenta; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G).  Size-selected >500bp
                     for average insert size 1.8kb.  Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

  Query Match             100.0%;  Score 90;  DB 12;  Length 588;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-15;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        459 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 518

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db        519 AAGCAGGGGGGAACGCTGGACGACCTAGAG 548


RESULT 2
BG107446
LOCUS       BG107446                589 bp    mRNA    linear   EST 30-JAN-2001
DEFINITION  602277558F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4365254 5',
            mRNA sequence.
ACCESSION   BG107446
VERSION     BG107446.1  GI:12601292
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 589)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10014  row: c  column: 15
            High quality sequence stop: 419.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4365254"
                     /tissue_type="osteosarcoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_86"
                     /note="Organ: bone; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
                     Average insert size 1.533 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             100.0%;  Score 90;  DB 12;  Length 589;
  Best Local Similarity   100.0%;  Pred. No. 7.2e-15;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         42 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 101

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db        102 AAGCAGGGGGGAACGCTGGACGACCTAGAG 131


RESULT 3
BE384533
LOCUS       BE384533                727 bp    mRNA    linear   EST 21-JUL-2000
DEFINITION  601277926F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3618751 5',
            mRNA sequence.
ACCESSION   BE384533
VERSION     BE384533.1  GI:9329898
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 727)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC/DCTD/DTP
             cDNA Library Preparation: Ling Hong/Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
            Plate: LLCM288  row: c  column: 08
            High quality sequence stop: 614.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:3618751"
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                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_20"
                     /note="Organ: skin; Vector: pOTB7; Site_1: XhoI; Site_2:
                     EcoRI; cDNA made by oligo-dT priming.  Directionally
                     cloned into EcoRI/XhoI sites using the following 5'
                     adaptor: GGCACGAG(G).  Size-selected >500bp for average
                     insert size 1.8kb.  Library constructed by Ling Hong in
                     the laboratory of Gerald M. Rubin (University of
                     California, Berkeley) using  ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies)."
ORIGIN

  Query Match             100.0%;  Score 90;  DB 10;  Length 727;
  Best Local Similarity   100.0%;  Pred. No. 7.8e-15;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        356 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 415

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db        416 AAGCAGGGGGGAACGCTGGACGACCTAGAG 445
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RESULT 4
BI084392
LOCUS       BI084392                745 bp    mRNA    linear   EST 20-JUN-2001
DEFINITION  602869515F1 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:5014442 5',
            mRNA sequence.
ACCESSION   BI084392
VERSION     BI084392.1  GI:14502722
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 745)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1821  row: m  column: 03
            High quality sequence stop: 744.
FEATURES             Location/Qualifiers
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                     /clone="IMAGE:5014442"
                     /tissue_type="epidermoid carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_102"
                     /note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G).  Library constructed
                     by Ling Hong in the laboratory of Gerald M. Rubin
                     (University of  California, Berkeley) using ZAP-cDNA
                     synthesis kit (Stratagene) and Superscript II RT (Life
                     Technologies). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match            100.0%;  Score 90;  DB 12;  Length 745;
  Best Local Similarity  100.0%;  Pred. No. 7.8e-15;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        180 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 239

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              |||||||||||||||||||||||||||||
Db        240 AAGCAGGGGGGAACGCTGGACGACCTAGAG 269


RESULT 5
CD251031
LOCUS       CD251031                868 bp    mRNA    linear   EST 22-MAY-2003
DEFINITION  AGENCOURT_14214315 NIH_MGC_179 Homo sapiens cDNA clone
            IMAGE:30385244 5', mRNA sequence.
ACCESSION   CD251031
VERSION     CD251031.1  GI:31011497
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 868)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM451  row: p  column: 21
            High quality sequence stop: 687.
FEATURES             Location/Qualifiers
     source          1. .868
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:30385244"
                     /tissue_type="Pituitary"
                     /lab_host="DH10B-Ton A ( T1 and T5 phage resistances)"
                     /clone_lib="NIH_MGC_179"
                     /note="Organ: brain; Vector: pCMV-SPORT6.1; Site_1: EcoRV
                     (destroyed); Site_2: NotI; Library is oligo-dT primed and
                     directionally cloned (EcoRV site is destroyed upon
                     cloning).  Average insert size 1.1 kb. Library was
                     constructed by (Invitrogen). Note: this is a NIH_MGC
                     Library."
ORIGIN

  Query Match            100.0%;  Score 90;  DB 14;  Length 868;
  Best Local Similarity  100.0%;  Pred. No. 8.3e-15;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        101 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 160

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              |||||||||||||||||||||||||||||
Db        161 AAGCAGGGGGGAACGCTGGACGACCTAGAG 190


RESULT 6
BU857051
LOCUS       BU857051                944 bp    mRNA    linear   EST 16-OCT-2002
DEFINITION  AGENCOURT_10480781 NIH_MGC_107 Homo sapiens cDNA clone
            IMAGE:6646854 5', mRNA sequence.
ACCESSION   BU857051
VERSION     BU857051.1  GI:24042041
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 944)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2886  row: f  column: 06
            High quality sequence stop: 718.
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FEATURES             Location/Qualifiers
     source          1. .944
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6646854"
                     /tissue_type="adenocarcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_107"
                     /note="Organ: breast; Vector: pOTB7; Site_1: EcoRI;
                     Site_2: XhoI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             100.0%;  Score 90;  DB 13;  Length 944;
  Best Local Similarity   100.0%;  Pred. No. 8.5e-15;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        213 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 272

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db        273 AAGCAGGGGGGAACGCTGGACGACCTAGAG 302


RESULT 7
BQ669894
LOCUS       BQ669894                974 bp    mRNA    linear   EST 15-JUL-2002
DEFINITION  AGENCOURT_8184827 NIH_MGC_102 Homo sapiens cDNA clone IMAGE:6257524
            5', mRNA sequence.
ACCESSION   BQ669894
VERSION     BQ669894.1  GI:21780728
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 974)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2411  row: p  column: 05
            High quality sequence stop: 527.
FEATURES             Location/Qualifiers
     source          1. .974
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6257524"
                     /tissue_type="epidermoid carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_102"
                     /note="Organ: salivary gland; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed
                     by Ling Hong in the laboratory of Gerald M. Rubin
                     (University of California, Berkeley) using ZAP-cDNA
                     synthesis kit (Stratagene) and Superscript II RT (Life
                     Technologies). Note: this is a NIH_MGC Library."
ORIGIN

  Query Match             100.0%;  Score 90;  DB 13;  Length 974;
  Best Local Similarity   100.0%;  Pred. No. 8.6e-15;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        178 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 237

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db        238 AAGCAGGGGGGAACGCTGGACGACCTAGAG 267


RESULT 8
AL542182/c
LOCUS       AL542182                1201 bp    mRNA    linear   EST 12-MAY-2003
DEFINITION  AL542182 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE008YM17
            3-PRIME, mRNA sequence.
ACCESSION   AL542182
VERSION     AL542182.2  GI:30547081
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1201)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     On Feb 15, 2001 this sequence version replaced gi:12873974.
            Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
            Library was constructed by Life Technologies, a division of
            Invitrogen. This sequence belongs to sequence cluster 4655.r For
            more information about this cluster, see
            http://www.genoscope.cns.fr/
            cgi-bin/cluster.cgi?seq=CS0DE008AG09NP1&cluster=4655.r. Contact :
            Feng Liang Email : fliang@lifetech.com URL :
            http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
            Faraday Avenue Genoscope sequence ID : CS0DE008AG09NP1.
FEATURES             Location/Qualifiers
     source          1. .1201
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="CS0DE008YM17"
                     /tissue_type="PLACENTA"
                     /clone_lib="Homo sapiens PLACENTA"
                     /note="Vector: pCMVSPORT_6; 1st strand cDNA was primed
                     with a NotI-oligo(dT) primer. Five prime end enriched,
                     double-strand cDNA was digested with Not I and cloned into
                     the Not I and EcoRV sites of the pCMVSPORT 6 vector.
                     Library was not normalized."
ORIGIN

  Query Match             100.0%;  Score 90;  DB 9;  Length 1201;
  Best Local Similarity   100.0%;  Pred. No. 9.2e-15;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        658 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 599

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db        598 AAGCAGGGGGGAACGCTGGACGACCTAGAG 569
```

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RESULT 9
BQ877352
LOCUS       BQ877352                878 bp    mRNA    linear   EST 16-AUG-2002
DEFINITION  AGENCOURT_8072483 NIH_MGC_110 Homo sapiens cDNA clone IMAGE:6084011
            5', mRNA sequence.
ACCESSION   BQ877352
VERSION     BQ877352.1  GI:22269360
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 878)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Rubin Laboratory
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM2315  row: b  column: 12
            High quality sequence stop: 621.
FEATURES             Location/Qualifiers
     source          1. .878
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6084011"
                     /tissue_type="ductal carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_110"
                     /note="Organ: pancreas; Vector: pOTB7; Site_1: XhoI;
                     Site_2: EcoRI; cDNA made by oligo-dT priming.
                     Directionally cloned into EcoRI/XhoI sites using the
                     following 5' adaptor: GGCACGAG(G). Library constructed by
                     Ling Hong in the laboratory of Gerald M. Rubin (University
                     of California, Berkeley) using ZAP-cDNA synthesis kit
                     (Stratagene) and Superscript II RT (Life Technologies).
                     Note: this is a NIH_MGC Library."
ORIGIN

  Query Match            98.2%;  Score 88.4;  DB 13;  Length 878;
  Best Local Similarity  98.9%;  Pred. No. 2.3e-14;
  Matches   89;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        551 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 610

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              |||||||||||||||||||||||||| ||
Db        611 AAGCAGGGGGGAACGCTGGACGACCTAAAG 640


RESULT 10
BF590924/c
LOCUS       BF590924                557 bp    mRNA    linear   EST 12-DEC-2000
DEFINITION  7h46b08.x1 NCI_CGAP_Co16 Homo sapiens cDNA clone IMAGE:3318999 3'
            similar to TR:O75327 O75327 IKB KINASE BETA SUBUNIT. [1] ;, mRNA
            sequence.
ACCESSION   BF590924
VERSION     BF590924.1  GI:11683248
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 557)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck,
            M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL, send email to:
            info@image.llnl.gov
            Seq primer: -40UP from Gibco
            High quality sequence stop: 402.
FEATURES             Location/Qualifiers
     source          1. .557
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3318999"
                     /tissue_type="colon tumor, RER+"
                     /lab_host="DH10B"
                     /clone_lib="NCI_CGAP_Co16"
                     /note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a
                     modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Plasmid DNA from the normalized library NCI_CGAP_Co10 was
                     prepared, and ss circles were made in vitro. Following HAP
                     purification, this DNA was used as tracer in a subtractive
                     hybridization reaction. The driver was PCR-amplified cDNAs
                     from a pool of 5,000 clones made from the same library
                     (cloneIDs 1057416-1061255, and 1144584-1145351).
                     Subtraction by Bento Soares and M. Fatima Bonaldo.  "
ORIGIN

  Query Match            96.4%;  Score 86.8;  DB 10;  Length 557;
  Best Local Similarity  97.8%;  Pred. No. 5.5e-14;
  Matches   88;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        332 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAAAGGAGCCCCATGGGCCGG 273

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              |||||||||||||||||||| ||||||||||
Db        272 AAGCAGGGGGGAACGCTGGTCGACCTAGAG 243


RESULT 11
BE077902
LOCUS       BE077902                402 bp    mRNA    linear   EST 09-JUN-2000
DEFINITION  CM1-BT0614-110300-142-c10 BT0614 Homo sapiens cDNA, mRNA sequence.
ACCESSION   BE077902
VERSION     BE077902.1  GI:8429180
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 402)
  AUTHORS   Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
            Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
            Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
            Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
            O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
            Simpson,A.J.
  TITLE     Shotgun sequencing of the human transcriptome with ORF expressed
            sequence tags
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
  MEDLINE   20202663
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   PUBMED   10737800
COMMENT     Contact: Simpson A.J.G.
            Laboratory of Cancer Genetics
            Ludwig Institute for Cancer Research
            Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
            Brazil
            Tel: +55-11-2704922
            Fax: +55-11-2707001
            Email: asimpson@ludwig.org.br
            This sequence was derived from the FAPESP/LICR Human Cancer Genome
            Project. This entry can be seen in the following URL
            (http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=CM1-BT0614-110
            300-142-c10&t3=2000-03-11&t4=1)
            Seq primer: puc 18 forward
            High quality sequence start: 8
            High quality sequence stop: 402.
FEATURES             Location/Qualifiers
     source          1. .402
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /dev_stage="Adult"
                     /clone_lib="BT0614"
                     /note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2:
                     SmaI; A mini-library was made by cloning products derived
                     from  ORESTES PCR (U.S. Letters Patent application No.
                     196,716 -  Ludwig Institute for Cancer Research) profiles
                     into  the pUC 18 vector. Reverse transcription of tissue
                     mRNA and cDNA amplification were performed under low
                     stringency conditions."
ORIGIN

  Query Match             95.6%;  Score 86;  DB 10;  Length 402;
  Best Local Similarity   100.0%;  Pred. No. 8.2e-14;
  Matches   86;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        109 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 168

Qy         61 AAGCAGGGGGGAACGCTGGACGACCT 86
              |||||||||||||||||||||||||
Db        169 AAGCAGGGGGGAACGCTGGACGACCT 194


RESULT 12
AQ827088/c
LOCUS       AQ827088                501 bp    DNA     linear   GSS 27-AUG-1999
DEFINITION  HS_5291_B1_H08_T7A RPCI-11 Human Male BAC Library Homo sapiens
            genomic clone Plate=867 Col=15 Row=P, genomic survey sequence.
ACCESSION   AQ827088
VERSION     AQ827088.1  GI:5793150
KEYWORDS    GSS.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 501)
  AUTHORS   Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
            Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
            Hood,L.
  TITLE     Sequence-tagged connectors: A sequence approach to mapping and
            scanning the human genome
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
  MEDLINE   99380589
   PUBMED   10449764
COMMENT     Contact: Mahairas GG, Wallace JC, Hood L
            High Throughput Sequencing Center
            University of Washington
            401 Queen Anne Avenue North, Seattle, WA 98109, USA
            Tel: (206) 616-3618
            Fax: (206) 616-3887
            Email: jwallace@u.washington.edu
            Clones are derived from the human BAC library RPCI-11. For BAC
            library availability, please contact Pieter de Jong
            (pieter@dejong.med.buffalo.edu). Clones may be purchased from
            BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
            or from Resear h Genetics (info@resgen.com). BAC end Web Server:
            http://www.htsc.washington.edu
            Plate: 867  row: P  column: 15
            Seq primer: T7
            Class: BAC ends
            High quality sequence stop: 501.
FEATURES             Location/Qualifiers
     source          1. .501
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
                     /clone="Plate=867 Col=15 Row=P"
                     /sex="male"
                     /clone_lib="RPCI-11 Human Male BAC Library"
                     /note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;
                     Male blood DNA was isolated from one randomly chosen donor
                     and partially digested with a combination of EcoRI and
                     EcoRI Methylase. Size selected DNA was cloned into the
                     pBACe3.6 vector at EcoRI sites"
ORIGIN

  Query Match             95.6%;  Score 86;  DB 28;  Length 501;
  Best Local Similarity   100.0%;  Pred. No. 8.9e-14;
  Matches   86;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        329 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 270

Qy         61 AAGCAGGGGGGAACGCTGGACGACCT 86
              |||||||||||||||||||||||||
Db        269 AAGCAGGGGGGAACGCTGGACGACCT 244


RESULT 13
CD299893
LOCUS       CD299893                864 bp    mRNA    linear   EST 27-MAY-2003
DEFINITION  AGENCOURT_14251668 NIH_MGC_180 Homo sapiens cDNA clone
            IMAGE:30388043 5', mRNA sequence.
ACCESSION   CD299893
VERSION     CD299893.1  GI:31079688
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 864)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Michael Brownstein
             cDNA Library Preparation: Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDAM459  row: e  column: 12
            High quality sequence stop: 566.
FEATURES             Location/Qualifiers
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                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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/clone="IMAGE:30388043"
/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
/clone_lib="NIH_MGC_180"
/note="Organ: Testis; Vector: pCMV-SPORT6.1; Site_1: NotI; Site_2: EcoRV (destroyed); Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.68 kb. Library was constructed by (Invitrogen). Note: this is a NIH_MGC Library."

ORIGIN

Query Match 95.6%; Score 86; DB 14; Length 864;
Best Local Similarity 100.0%; Pred. No. 1.1e-13;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 AAGCAGGGGGGAACGCTGGACGACCT 86
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RESULT 14
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LOCUS AI906358 400 bp mRNA linear EST 30-MAR-2000
DEFINITION RC-BT108-040399-031 BT108 Homo sapiens cDNA, mRNA sequence.
ACCESSION AI906358
VERSION AI906358.1 GI:6496745
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 400)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/seq/gethtml.pl?t1=RC&t2=RC-BT108-031.html&t3=040399&t4=1)
Seq primer: puc 18 forward.

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/db_xref="taxon:9606"
/sex="female"
/dev_stage="Adult"
/clone_lib="BT108"
/note="Organ: breast; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 90.7%; Score 81.6; DB 9; Length 400;
Best Local Similarity 95.5%; Pred. No. 1.4e-12;
Matches 84; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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RESULT 15
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LOCUS AW997999 401 bp mRNA linear EST 05-JUN-2000
DEFINITION RC1-BN0056-230200-021-b11 BN0056 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW997999
VERSION AW997999.1 GI:8258233
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 401)
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R., Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F., Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H., Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and Simpson,A.J.
TITLE Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE 20202663
PUBMED 10737800
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1=&t2=RC1-BN0056-230200-021-b11&t3=2000-02-23&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 15
High quality sequence stop: 401.

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/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BN0056"
/note="Organ: breast_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

ORIGIN

Query Match 87.8%; Score 79; DB 10; Length 401;
Best Local Similarity 98.9%; Pred. No. 7.3e-12;

Matches 90; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Qy         60 GAAGCAGGGGGGAACGCTGGACGACCTAGAG 90
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Search completed: September 23, 2004, 21:02:15
Job time : 2495 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 19:41:56 ; Search time 369 Seconds
(without alignments)
135.354 Million cell updates/sec

Title: US-09-806-701-15_COPY_991_1080
Perfect score: 90
Sequence: 1 gaacggatgatggctctgca.....gaacgctggacgacctagag 90

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/2/ina/5B_COMB.seq:*
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5: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	90	100.0	1055	3	US-09-215-131-3	Sequence 3, Appli
2	90	100.0	1055	3	US-09-222-734-3	Sequence 3, Appli
3	90	100.0	2268	2	US-08-890-853-1	Sequence 1, Appli
4	90	100.0	2268	2	US-09-099-125A-1	Sequence 1, Appli
5	90	100.0	2268	2	US-09-099-124A-1	Sequence 1, Appli
6	90	100.0	2268	2	US-09-197-008-1	Sequence 1, Appli
7	90	100.0	2268	3	US-09-032-476-1	Sequence 1, Appli
8	90	100.0	2268	3	US-08-890-854-1	Sequence 1, Appli
9	90	100.0	2268	3	US-09-023-324-1	Sequence 1, Appli
10	90	100.0	2268	4	US-09-109-986-1	Sequence 1, Appli
11	90	100.0	2271	3	US-08-910-820-8	Sequence 8, Appli
12	90	100.0	2271	4	US-09-844-908-8	Sequence 8, Appli
13	90	100.0	2931	3	US-09-168-629-14	Sequence 14, Appl
14	90	100.0	3966	3	US-09-215-131-1	Sequence 1, Appli
15	90	100.0	3966	3	US-09-222-734-1	Sequence 1, Appli
16	35.6	39.6	1874	4	US-09-536-882A-6	Sequence 6, Appli
17	35.6	39.6	2025	3	US-09-160-483-2	Sequence 2, Appli
18	35.6	39.6	3314	4	US-09-536-882A-5	Sequence 5, Appli
19	34.6	38.4	2146	3	US-09-032-476-5	Sequence 5, Appli
20	34.6	38.4	2146	3	US-08-890-854-5	Sequence 5, Appli
21	34.6	38.4	2146	3	US-09-023-324-5	Sequence 5, Appli
22	34.6	38.4	2146	4	US-09-109-986-5	Sequence 5, Appli
23	34.6	38.4	2238	2	US-08-890-853-3	Sequence 3, Appli
24	34.6	38.4	2238	2	US-09-099-125A-3	Sequence 3, Appli
25	34.6	38.4	2238	2	US-09-099-124A-3	Sequence 3, Appli
26	34.6	38.4	2238	3	US-09-032-476-3	Sequence 3, Appli
27	34.6	38.4	2238	3	US-08-890-854-3	Sequence 3, Appli
28	34.6	38.4	2238	3	US-09-023-324-3	Sequence 3, Appli
29	34.6	38.4	2238	4	US-09-109-986-3	Sequence 3, Appli
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31	34.6	38.4	2251	4	US-09-844-908-7	Sequence 7, Appli
32	34.6	38.4	2273	3	US-09-168-629-1	Sequence 1, Appli
33	34.6	38.4	2273	3	US-08-810-131A-1	Sequence 1, Appli
34	33	36.7	2273	2	US-09-197-360-1	Sequence 1, Appli
35	33	36.7	2273	4	US-09-856-074B-1	Sequence 1, Appli
36	33	36.7	2991	4	US-09-417-197-122	Sequence 122, App
37	33	36.7	2994	4	US-09-417-197-120	Sequence 120, App
c 38	30.2	33.6	909	4	US-09-252-991A-15957	Sequence 15957, A
39	30.2	33.6	1221	4	US-09-252-991A-16324	Sequence 16324, A
40	29.2	32.4	1074	2	US-08-463-081B-29	Sequence 29, Appl
41	29.2	32.4	1074	2	US-08-461-379A-29	Sequence 29, Appl
42	29.2	32.4	1074	2	US-08-462-390B-29	Sequence 29, Appl
43	29.2	32.4	1074	3	US-08-463-074B-29	Sequence 29, Appl
44	29.2	32.4	1074	3	US-08-465-585C-29	Sequence 29, Appl
45	29.2	32.4	1074	3	US-08-652-446-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-09-215-131-3
; Sequence 3, Application US/09215131
; Patent No. 6030834
; GENERAL INFORMATION:
; APPLICANT: Chu, Keting
; APPLICANT: Pot, David
; TITLE OF INVENTION: IKK Beta Regulates Transcription Factors
; FILE REFERENCE: 1449.002
; CURRENT APPLICATION NUMBER: US/09/215,131
; CURRENT FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 1055
; TYPE: DNA
; ORGANISM: human
US-09-215-131-3

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Best Local Similarity 100.0%; Pred. No. 1.7e-20;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
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Db        382 AAGCAGGGGGGAACGCTGGACGACCTAGAG 411
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RESULT 2
US-09-222-734-3
; Sequence 3, Application US/09222734A
; Patent No. 6077701
; GENERAL INFORMATION:
; APPLICANT: Chu, Keting
; APPLICANT: Pot, David
; TITLE OF INVENTION: IKK-beta Regulates Transcription Factors
; FILE REFERENCE: 12441.78080
; CURRENT APPLICATION NUMBER: US/09/222,734A
; CURRENT FILING DATE: 1998-12-29
; EARLIER APPLICATION NUMBER: 09/215,131
; EARLIER FILING DATE: 1998-12-18
; EARLIER APPLICATION NUMBER: 60/068,954
; EARLIER FILING DATE: 1997-12-30
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3

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;   LENGTH: 1055
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-222-734-3

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  Best Local Similarity   100.0%;  Pred. No. 1.7e-20;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
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Db        322 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 381

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
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Db        382 AAGCAGGGGGGAACGCTGGACGACCTAGAG 411


RESULT 3
US-08-890-853-1
; Sequence 1, Application US/08890853
; Patent No. 5851812
;  GENERAL INFORMATION:
;    APPLICANT:  Goeddel, David V.
;    APPLICANT:  Woronicz, John
;    TITLE OF INVENTION:  IKK-  Proteins, Nucleic Acids and Methods
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  268 BUSH STREET, SUITE 3200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/890,853
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  T97-006-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 343-4341
;      TELEFAX:  (415) 343-4342
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2268 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-08-890-853-1

  Query Match             100.0%;  Score 90;  DB 2;  Length 2268;
  Best Local Similarity   100.0%;  Pred. No. 2e-20;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
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Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 4
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US-09-099-125A-1
; Sequence 1, Application US/09099125A
; Patent No. 5916760
;  GENERAL INFORMATION:
;    APPLICANT:  Goeddel, David V.
;    APPLICANT:  Woronicz, John
;    TITLE OF INVENTION:  IKK-  Proteins, Nucleic Acids and Methods
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  268 BUSH STREET, SUITE 3200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/099,125A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/890,853
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  T97-006-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 343-4341
;      TELEFAX:  (415) 343-4342
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2268 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-099-125A-1

  Query Match             100.0%;  Score 90;  DB 2;  Length 2268;
  Best Local Similarity   100.0%;  Pred. No. 2e-20;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
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Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 5
US-09-099-124A-1
; Sequence 1, Application US/09099124A
; Patent No. 5939302
;  GENERAL INFORMATION:
;    APPLICANT:  Goeddel, David V.
;    APPLICANT:  Woronicz, John
;    TITLE OF INVENTION:  IKK-  Proteins, Nucleic Acids and Methods
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  268 BUSH STREET, SUITE 3200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
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;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/099,124A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/890,853
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  T97-006-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 343-4341
;      TELEFAX:  (415) 343-4342
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2268 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-099-124A-1

  Query Match             100.0%;  Score 90;  DB 2;  Length 2268;
  Best Local Similarity   100.0%;  Pred. No. 2e-20;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGGAACGCTGGACGACCTAGAG 90
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Db       1663 AAGCAGGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 6
US-09-197-008-1
; Sequence 1, Application US/09197008
; Patent No. 5977341
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT: Lex M. Cowsert
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-BETA EXPRESSION
;  FILE REFERENCE: RTS-0019
;  CURRENT APPLICATION NUMBER: US/09/197,008
;  CURRENT FILING DATE: 1998-11-20
;  NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
;   LENGTH: 2268
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2268)
US-09-197-008-1

  Query Match             100.0%;  Score 90;  DB 2;  Length 2268;
  Best Local Similarity   100.0%;  Pred. No. 2e-20;
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Qy         61 AAGCAGGGGGGGAACGCTGGACGACCTAGAG 90
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Db       1663 AAGCAGGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 7
US-09-032-476-1
; Sequence 1, Application US/09032476
; Patent No. 6235492
;  GENERAL INFORMATION:
;    APPLICANT:  Rothe, Mike
;    APPLICANT:  Cao, Zhaodan
;    APPLICANT:  R gnier, Catherine
;    TITLE OF INVENTION:  IKK-` Proteins, Nucleic Acids and Methods
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  268 BUSH STREET, SUITE 3200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/032,476
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/890,854
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  T97-006-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 343-4341
;      TELEFAX:  (415) 343-4342
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2268 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-032-476-1

  Query Match             100.0%;  Score 90;  DB 3;  Length 2268;
  Best Local Similarity   100.0%;  Pred. No. 2e-20;
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Qy         61 AAGCAGGGGGGGAACGCTGGACGACCTAGAG 90
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RESULT 8
US-08-890-854-1
; Sequence 1, Application US/08890854
; Patent No. 6235512
;  GENERAL INFORMATION:
;    APPLICANT:  Rothe, Mike
;    APPLICANT:  Cao, Zhaodan
;    APPLICANT:  R gnier, Catherine
;    TITLE OF INVENTION:  IKK-` Proteins, Nucleic Acids and Methods
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  268 BUSH STREET, SUITE 3200
;      CITY:  SAN FRANCISCO
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;       STATE:  CALIFORNIA
;       COUNTRY:  USA
;       ZIP:  94104
;     COMPUTER READABLE FORM:
;       MEDIUM TYPE:  Floppy disk
;       COMPUTER:  IBM PC compatible
;       OPERATING SYSTEM:  PC-DOS/MS-DOS
;       SOFTWARE:  PatentIn Release #1.0, Version #1.30
;     CURRENT APPLICATION DATA:
;       APPLICATION NUMBER:  US/08/890,854
;       FILING DATE:
;       CLASSIFICATION:  435
;     ATTORNEY/AGENT INFORMATION:
;       NAME:  OSMAN, RICHARD A
;       REGISTRATION NUMBER:  36,627
;       REFERENCE/DOCKET NUMBER:  T97-006-1
;     TELECOMMUNICATION INFORMATION:
;       TELEPHONE:  (415) 343-4341
;       TELEFAX:  (415) 343-4342
;   INFORMATION FOR SEQ ID NO:  1:
;     SEQUENCE CHARACTERISTICS:
;       LENGTH:  2268 base pairs
;       TYPE:  nucleic acid
;       STRANDEDNESS:  double
;       TOPOLOGY:  linear
;     MOLECULE TYPE:  cDNA
US-08-890-854-1

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Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
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Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 9
US-09-023-324-1
; Sequence 1, Application US/09023324
; Patent No. 6235513
;  GENERAL INFORMATION:
;    APPLICANT:  Rothe, Mike
;    APPLICANT:  Cao, Zhaodan
;    APPLICANT:  R gnier, Catherine
;    TITLE OF INVENTION:  IKK-` Proteins, Nucleic Acids and Methods
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  268 BUSH STREET, SUITE 3200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,324
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;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/890,854
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  T97-006-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 343-4341
;      TELEFAX:  (415) 343-4342
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2268 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-023-324-1

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Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
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Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 10
US-09-109-986-1
; Sequence 1, Application US/09109986
; Patent No. 6479266
;  GENERAL INFORMATION:
;    APPLICANT:  Rothe, Mike
;    APPLICANT:  Cao, Zhaodan
;    APPLICANT:  R gnier, Catherine
;    TITLE OF INVENTION:  IKK-` Proteins, Nucleic Acids and Methods
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  268 BUSH STREET, SUITE 3200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
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;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
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;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/890,854
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  T97-006-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 343-4341
;      TELEFAX:  (415) 343-4342
;  INFORMATION FOR SEQ ID NO:  1:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2268 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  double
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  cDNA
US-09-109-986-1

  Query Match             100.0%;  Score 90;  DB 4;  Length 2268;
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Qy         61 AAGCAGGGGGGGAACGCTGGACGACCTAGAG 90
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Db       1663 AAGCAGGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 11
US-08-910-820-8
; Sequence 8, Application US/08910820
; Patent No. 6258579
;  GENERAL INFORMATION:
;    APPLICANT:  Mercurio, Frank
;    APPLICANT:  Zhu, Hengyi
;    APPLICANT:  Barbosa, Miguel
;    APPLICANT:  Li, Gian
;    APPLICANT:  Murray, Brion W.
;    TITLE OF INVENTION:  STIMULUS-INDUCIBLE PROTEIN KINASE
;    TITLE OF INVENTION:  COMPLEX AND METHODS OF USE THEREFOR
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,820
;      FILING DATE:  12-AUG-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  860098.413C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  8:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  2271 base pairs
;      TYPE:  nucleic acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
US-08-910-820-8

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Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGGAACGCTGGACGACCTAGAG 90
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Db       1663 AAGCAGGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 12
US-09-844-908-8
; Sequence 8, Application US/09844908
; Patent No. 6576437
;  GENERAL INFORMATION:
;       APPLICANT: Mercurio, Frank
;                  Zhu, Hengyi
;                  Barbosa, Miguel
;                  Li, Gian
;                  Murray, Brion W.
;       TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
;                           COMPLEX AND METHODS OF USE THEREFOR
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: SEED and BERRY LLP
;            STREET: 6300 Columbia Center, 701 Fifth Avenue
;            CITY: Seattle
;            STATE: Washington
;            COUNTRY: USA
;            ZIP: 98104
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
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;            FILING DATE: 27-Apr-2001
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/08/910,820
;            FILING DATE: 12-AUG-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Maki, David J.
;            REGISTRATION NUMBER: 31,392
;            REFERENCE/DOCKET NUMBER: 860098.413C1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (206) 622-4900
;            TELEFAX: (206) 682-6031
;  INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2271 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-844-908-8

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RESULT 13
US-09-168-629-14
; Sequence 14, Application US/09168629
; Patent No. 6242253
; GENERAL INFORMATION:
;  APPLICANT: Karin, Michael
;  APPLICANT: DiDonato, Joseph A.
;  APPLICANT: Rothwarf, David M.
;  APPLICANT: Hayakawa, Makio
;  APPLICANT: Zandi, Ebrahim
;  TITLE OF INVENTION: IkB Kinase, Subunits Thereof, and Methods of Using Same
;  FILE REFERENCE: P-UD 3295
;  CURRENT APPLICATION NUMBER: US/09/168,629
;  CURRENT FILING DATE: 1998-10-08
;  EARLIER APPLICATION NUMBER: 60/061,470
;  EARLIER FILING DATE: 1997-10-09
;  NUMBER OF SEQ ID NOS: 20
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;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 2931
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (36)..(2306)
US-09-168-629-14

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RESULT 14
US-09-215-131-1
; Sequence 1, Application US/09215131
; Patent No. 6030834
; GENERAL INFORMATION:
;  APPLICANT: Chu, Keting
;  APPLICANT: Pot, David
;  TITLE OF INVENTION: IKK Beta Regulates Transcription Factors
;  FILE REFERENCE: 1449.002
;  CURRENT APPLICATION NUMBER: US/09/215,131
;  CURRENT FILING DATE: 1998-12-18
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 1
;   LENGTH: 3966
;   TYPE: DNA
;   ORGANISM: human
US-09-215-131-1

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Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
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Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 15
US-09-222-734-1
; Sequence 1, Application US/09222734A
; Patent No. 6077701
; GENERAL INFORMATION:
;  APPLICANT: Chu, Keting
;  APPLICANT: Pot, David
;  TITLE OF INVENTION: IKK-beta Regulates Transcription Factors
;  FILE REFERENCE: 12441.78080
;  CURRENT APPLICATION NUMBER: US/09/222,734A
;  CURRENT FILING DATE: 1998-12-29
;  EARLIER APPLICATION NUMBER: 09/215,131
;  EARLIER FILING DATE: 1998-12-18
;  EARLIER APPLICATION NUMBER: 60/068,954
;  EARLIER FILING DATE: 1997-12-30
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 3966
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-09-222-734-1

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              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
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GenCore version 5.1.6

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Searched: 3337386 seqs, 2532474682 residues

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Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	90	100.0	2268	10	US-09-847-946A-1	Sequence 1, Appli
4	90	100.0	2268	15	US-10-156-610-1	Sequence 1, Appli
5	90	100.0	2268	15	US-10-243-408-1	Sequence 1, Appli
6	90	100.0	2271	9	US-09-844-908-8	Sequence 8, Appli
7	90	100.0	2271	9	US-09-844-988-8	Sequence 8, Appli
8	90	100.0	2271	15	US-10-338-462-8	Sequence 8, Appli
9	90	100.0	2931	9	US-09-796-872-14	Sequence 14, Appl
10	90	100.0	4154	13	US-10-087-192-1757	Sequence 1757, Ap
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12	77.2	85.8	3038	15	US-10-156-610-83	Sequence 83, Appl
13	74	82.2	2274	15	US-10-156-610-48	Sequence 48, Appl
14	74	82.2	3210	13	US-10-087-192-1754	Sequence 1754, Ap
15	70	77.8	67076	13	US-10-087-192-1753	Sequence 1753, Ap
16	35.6	39.6	1875	15	US-10-188-937A-6	Sequence 6, Appli
17	35.6	39.6	3314	15	US-10-188-937A-5	Sequence 5, Appli
18	34.6	38.4	2146	15	US-10-243-408-5	Sequence 5, Appli
19	34.6	38.4	2238	15	US-10-243-408-3	Sequence 3, Appli
20	34.6	38.4	2251	9	US-09-844-908-7	Sequence 7, Appli
21	34.6	38.4	2251	9	US-09-844-988-7	Sequence 7, Appli
22	34.6	38.4	2251	15	US-10-338-462-7	Sequence 7, Appli
23	34.6	38.4	2273	9	US-09-796-872-1	Sequence 1, Appli
24	34.6	38.4	3525	15	US-10-101-510-632	Sequence 632, App
25	34.6	38.4	3618	17	US-10-741-601-91	Sequence 91, Appl
26	33.6	37.3	53328	17	US-10-741-601-5639	Sequence 5639, Ap
27	33	36.7	2273	15	US-10-145-857-1	Sequence 1, Appli
28	33	36.7	2991	15	US-10-072-036-122	Sequence 122, App
29	33	36.7	2994	15	US-10-072-036-120	Sequence 120, App
c 30	30.6	34.0	649	13	US-10-027-632-115364	Sequence 115364,
c 31	30.6	34.0	649	13	US-10-027-632-115365	Sequence 115365,
c 32	30.6	34.0	649	13	US-10-027-632-115366	Sequence 115366,
c 33	30.6	34.0	649	16	US-10-027-632-115364	Sequence 115364,
c 34	30.6	34.0	649	16	US-10-027-632-115365	Sequence 115365,
c 35	30.6	34.0	649	16	US-10-027-632-115366	Sequence 115366,
36	30.6	34.0	715	13	US-10-425-114-18909	Sequence 18909, A
37	30.6	34.0	993	17	US-10-389-566-188	Sequence 188, App
38	30.2	33.6	1087	17	US-10-437-963-44491	Sequence 44491, A
39	30.2	33.6	1754	17	US-10-437-963-44490	Sequence 44490, A
40	29.8	33.1	3471	16	US-10-369-493-45054	Sequence 45054, A
41	29.4	32.7	366	15	US-10-156-761-2009	Sequence 2009, Ap
c 42	29.4	32.7	9025608	15	US-10-156-761-1	Sequence 1, Appli
43	29.2	32.4	780	17	US-10-437-963-3953	Sequence 3953, Ap
44	29.2	32.4	1077	11	US-09-826-509-558	Sequence 558, App
45	29.2	32.4	1345	9	US-09-853-450-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1
US-09-918-995-24344
; Sequence 24344, Application US/09918995
; Publication No. US20030073623A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc.
; TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
; TITLE OF INVENTION: FROM VARIOUS cDNA LIBRARIES
; FILE REFERENCE: 20411-756
; CURRENT APPLICATION NUMBER: US/09/918,995
; CURRENT FILING DATE: 2001-07-30
; PRIOR APPLICATION NUMBER: US/09/235,076
; PRIOR FILING DATE: 1999-01-20
; NUMBER OF SEQ ID NOS: 38054
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24344
; LENGTH: 506
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(506)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-24344

Query Match 100.0%; Score 90; DB 10; Length 506;
Best Local Similarity 100.0%; Pred. No. 1.1e-21;
Matches 90; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 64 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 123

Qy 61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
||||||||||||||||||||||||||||||
Db 124 AAGCAGGGGGGAACGCTGGACGACCTAGAG 153

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RESULT 2
US-10-106-698-455
; Sequence 455, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
;  APPLICANT: Ruben et al.
;  TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
;  FILE REFERENCE: PA005P1
;  CURRENT APPLICATION NUMBER: US/10/106,698
;  CURRENT FILING DATE:  2002-03-27
;  PRIOR APPLICATION NUMBER: PCT/US00/26524
;  PRIOR FILING DATE: 2000-09-28
;  PRIOR APPLICATION NUMBER: US 60/157,137
;  PRIOR FILING DATE: 1999-09-29
;  PRIOR APPLICATION NUMBER: US 60/163,280
;  PRIOR FILING DATE: 1999-11-03
;  NUMBER OF SEQ ID NOS: 8564
;  SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 455
;   LENGTH: 1558
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (420)..(420)
;   OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-455

  Query Match             100.0%;  Score 90;  DB 15;  Length 1558;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-21;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        817 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 876

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db        877 AAGCAGGGGGGAACGCTGGACGACCTAGAG 906


RESULT 3
US-09-847-946A-1
; Sequence 1, Application US/09847946A
; Publication No. US20030054999A1
; GENERAL INFORMATION:
;  APPLICANT: May, Michael J
;  APPLICANT:  Ghosh, Sankar
;  APPLICANT:  Findeis, Mark A
;  APPLICANT:  Phillips, Kathryn
;  APPLICANT:  Hannig, Gerhard
;  TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOUNDS AND USES THEREOF
;  FILE REFERENCE: PPI-119
;  CURRENT APPLICATION NUMBER: US/09/847,946A
;  CURRENT FILING DATE:  2001-05-02
;  PRIOR APPLICATION NUMBER: 60/201,261
;  PRIOR FILING DATE: 2000-05-02
;  PRIOR APPLICATION NUMBER: 09/643,260
;  PRIOR FILING DATE: 2000-08-22
;  NUMBER OF SEQ ID NOS: 160
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 2268
;   TYPE: DNA
;   ORGANISM: Artificial Sequence
;   FEATURE:
;   OTHER INFORMATION: Description of Artificial Sequence:wild-type IKK(
;   OTHER INFORMATION: NBD
US-09-847-946A-1

  Query Match             100.0%;  Score 90;  DB 10;  Length 2268;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-21;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 4
US-10-156-610-1
; Sequence 1, Application US/10156610
; Publication No. US20030050270A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Lex M. Cowsert
;  APPLICANT:  Erich Koller
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-BETA EXPRESSION
;  FILE REFERENCE: ISPH-0666
;  CURRENT APPLICATION NUMBER: US/10/156,610
;  CURRENT FILING DATE:  2002-05-24
;  PRIOR APPLICATION NUMBER: US 09/856,246
;  PRIOR FILING DATE: 2001-08-30
;  PRIOR APPLICATION NUMBER: PCT/US99/16959
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: US 09/197,008
;  PRIOR FILING DATE: 1998-11-20
;  NUMBER OF SEQ ID NOS: 83
; SEQ ID NO 1
;   LENGTH: 2268
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (1)..(2268)
US-10-156-610-1

  Query Match             100.0%;  Score 90;  DB 15;  Length 2268;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-21;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 5
US-10-243-408-1
; Sequence 1, Application US/10243408
; Publication No. US20030077683A1
;   GENERAL INFORMATION:
;        APPLICANT: Rothe, Mike
;                   Cao, Zhaodan
;                   R gnier, Catherine
;        TITLE OF INVENTION: IKK-' Proteins, Nucleic Acids and Methods
;        NUMBER OF SEQUENCES: 5
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;             STREET: 268 BUSH STREET, SUITE 3200
;             CITY: SAN FRANCISCO
;             STATE: CALIFORNIA
;             COUNTRY: USA
;             ZIP: 94104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
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;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;          CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/243,408
;             FILING DATE: 13-Sep-2002
;             CLASSIFICATION: <Unknown>
;          PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/109,986
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/890,854
;             FILING DATE: <Unknown>
;          ATTORNEY/AGENT INFORMATION:
;             NAME: OSMAN, RICHARD A
;             REGISTRATION NUMBER: 36,627
;             REFERENCE/DOCKET NUMBER: T97-006-1
;          TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 343-4341
;             TELEFAX: (415) 343-4342
;       INFORMATION FOR SEQ ID NO: 1:
;          SEQUENCE CHARACTERISTICS:
;             LENGTH: 2268 base pairs
;             TYPE: nucleic acid
;             STRANDEDNESS: double
;             TOPOLOGY: linear
;          MOLECULE TYPE: cDNA
;          SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-243-408-1

  Query Match             100.0%;  Score 90;  DB 15;  Length 2268;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-21;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 6
US-09-844-908-8
; Sequence 8, Application US/09844908
; Patent No. US20020151021A1
;   GENERAL INFORMATION:
;       APPLICANT: Mercurio, Frank
;                  Zhu, Hengyi
;                  Barbosa, Miguel
;                  Li, Gian
;                  Murray, Brion W.
;       TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
;                           COMPLEX AND METHODS OF USE THEREFOR
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;          ADDRESSEE: SEED and BERRY LLP
;          STREET: 6300 Columbia Center, 701 Fifth Avenue
;          CITY: Seattle
;          STATE: Washington
;          COUNTRY: USA
;          ZIP: 98104
;       COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: IBM PC compatible
;          OPERATING SYSTEM: PC-DOS/MS-DOS
;          SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/09/844,908
;          FILING DATE: 27-Apr-2001
;          CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: US/08/910,820
;          FILING DATE: 12-AUG-1997
;       ATTORNEY/AGENT INFORMATION:
;          NAME: Maki, David J.
;          REGISTRATION NUMBER: 31,392
;          REFERENCE/DOCKET NUMBER: 860098.413C1
;       TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (206) 622-4900
;          TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;          LENGTH: 2271 base pairs
;          TYPE: nucleic acid
;          STRANDEDNESS: single
;          TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-844-908-8

  Query Match             100.0%;  Score 90;  DB 9;  Length 2271;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-21;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 7
US-09-844-988-8
; Sequence 8, Application US/09844988
; Patent No. US20020158764A1
;   GENERAL INFORMATION:
;       APPLICANT: Mercurio, Frank
;                  Zhu, Hengyi
;                  Barbosa, Miguel
;                  Li, Gian
;                  Murray, Brion W.
;       TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
;                           COMPLEX AND METHODS OF USE THEREFOR
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;          ADDRESSEE: SEED and BERRY LLP
;          STREET: 6300 Columbia Center, 701 Fifth Avenue
;          CITY: Seattle
;          STATE: Washington
;          COUNTRY: USA
;          ZIP: 98104
;       COMPUTER READABLE FORM:
;          MEDIUM TYPE: Floppy disk
;          COMPUTER: IBM PC compatible
;          OPERATING SYSTEM: PC-DOS/MS-DOS
;          SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;          APPLICATION NUMBER: US/09/844,988
;          FILING DATE: 26-Apr-2001
;          CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;          APPLICATION NUMBER: 08/910,820
;          FILING DATE: 1997-08-13
;       ATTORNEY/AGENT INFORMATION:
;          NAME: Maki, David J.
;          REGISTRATION NUMBER: 31,392
;          REFERENCE/DOCKET NUMBER: 860098.413C1
;       TELECOMMUNICATION INFORMATION:
;          TELEPHONE: (206) 622-4900
;          TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;          LENGTH: 2271 base pairs
;          TYPE: nucleic acid
;          STRANDEDNESS: single
;          TOPOLOGY: linear
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;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-844-988-8

  Query Match             100.0%;  Score 90;  DB 9;  Length 2271;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-21;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 8
US-10-338-462-8
; Sequence 8, Application US/10338462
; Publication No. US20030100026A1
;   GENERAL INFORMATION:
;       APPLICANT: Mercurio, Frank
;                  Zhu, Hengyi
;                  Barbosa, Miguel
;                  Li, Gian
;                  Murray, Brion W.
;       TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
;                           COMPLEX AND METHODS OF USE THEREFOR
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: SEED and BERRY LLP
;            STREET: 6300 Columbia Center, 701 Fifth Avenue
;            CITY: Seattle
;            STATE: Washington
;            COUNTRY: USA
;            ZIP: 98104
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
;            OPERATING SYSTEM: PC-DOS/MS-DOS
;            SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;            APPLICATION NUMBER: US/10/338,462
;            FILING DATE: 08-Jan-2003
;            CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;            APPLICATION NUMBER: US/09/844,908
;            FILING DATE: 27-Apr-2001
;            APPLICATION NUMBER: US/08/910,820
;            FILING DATE: 12-AUG-1997
;       ATTORNEY/AGENT INFORMATION:
;            NAME: Maki, David J.
;            REGISTRATION NUMBER: 31,392
;            REFERENCE/DOCKET NUMBER: 860098.413C1
;       TELECOMMUNICATION INFORMATION:
;            TELEPHONE: (206) 622-4900
;            TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 8:
;       SEQUENCE CHARACTERISTICS:
;            LENGTH: 2271 base pairs
;            TYPE: nucleic acid
;            STRANDEDNESS: single
;            TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-10-338-462-8

  Query Match             100.0%;  Score 90;  DB 15;  Length 2271;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-21;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1603 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db       1663 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1692


RESULT 9
US-09-796-872-14
; Sequence 14, Application US/09796872
; Patent No. US20020045235A1
; GENERAL INFORMATION:
;  APPLICANT: Karin, Michael
;  APPLICANT:  DiDonato, Joseph A.
;  APPLICANT:  Rothwarf, David M.
;  APPLICANT:  Hayakawa, Makio
;  APPLICANT:  Zandi, Ebrahim
;  TITLE OF INVENTION: IkB Kinase, Subunits Thereof, and Methods of Using Same
;  FILE REFERENCE: P-UD 3295
;  CURRENT APPLICATION NUMBER: US/09/796,872
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER: 09/168,629
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/061,470
;  PRIOR FILING DATE: 1997-10-09
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 2931
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: CDS
;   LOCATION: (36)..(2306)
US-09-796-872-14

  Query Match             100.0%;  Score 90;  DB 9;  Length 2931;
  Best Local Similarity   100.0%;  Pred. No. 1.2e-21;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1638 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1697

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db       1698 AAGCAGGGGGGAACGCTGGACGACCTAGAG 1727


RESULT 10
US-10-087-192-1757
; Sequence 1757, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Engelhard, Eric K.
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
;  TITLE OF INVENTION:  CANCER
;  FILE REFERENCE: 529452000122
;  CURRENT APPLICATION NUMBER: US/10/087,192
;  CURRENT FILING DATE:  2002-03-01
;  PRIOR APPLICATION NUMBER: US 09/747,377
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 2059
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1757
;   LENGTH: 4154
;   TYPE: DNA
;   ORGANISM: Homo sapiens
US-10-087-192-1757

  Query Match             100.0%;  Score 90;  DB 13;  Length 4154;
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  Best Local Similarity   100.0%;  Pred. No. 1.2e-21;
  Matches   90;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1813 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 1872

Qy         61 AAGCAGGGGGGGAACGCTGGACGACCTAGAG 90
              ||||||||||||||||||||||||||||||
Db       1873 AAGCAGGGGGGGAACGCTGGACGACCTAGAG 1902


RESULT 11
US-10-087-192-1756
; Sequence 1756, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Engelhard, Eric K.
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
;  TITLE OF INVENTION:  CANCER
;  FILE REFERENCE: 529452000122
;  CURRENT APPLICATION NUMBER: US/10/087,192
;  CURRENT FILING DATE:  2002-03-01
;  PRIOR APPLICATION NUMBER: US 09/747,377
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 2059
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1756
;   LENGTH: 81099
;   TYPE: DNA
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: misc_feature
;   LOCATION: (1)...(81099)
;   OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1756

  Query Match             95.6%;  Score 86;  DB 13;  Length 81099;
  Best Local Similarity   100.0%;  Pred. No. 3.6e-20;
  Matches   86;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      59517 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 59576

Qy         61 AAGCAGGGGGGAACGCTGGACGACCT 86
              |||||||||||||||||||||||||||
Db      59577 AAGCAGGGGGGAACGCTGGACGACCT 59602


RESULT 12
US-10-156-610-83
; Sequence 83, Application US/10156610
; Publication No. US20030050270A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Lex M. Cowsert
;  APPLICANT:  Erich Koller
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-BETA EXPRESSION
;  FILE REFERENCE: ISPH-0666
;  CURRENT APPLICATION NUMBER: US/10/156,610
;  CURRENT FILING DATE:  2002-05-24
;  PRIOR APPLICATION NUMBER: US 09/856,246
;  PRIOR FILING DATE: 2001-08-30
;  PRIOR APPLICATION NUMBER: PCT/US99/16959
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: US 09/197,008
;  PRIOR FILING DATE: 1998-11-20
;  NUMBER OF SEQ ID NOS: 83
; SEQ ID NO 83
;   LENGTH: 3038
;   TYPE: DNA
;   ORGANISM: Rattus norvegicus
US-10-156-610-83

  Query Match             85.8%;  Score 77.2;  DB 15;  Length 3038;
  Best Local Similarity   91.1%;  Pred. No. 3.5e-17;
  Matches   82;  Conservative    0;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              |||||||||||||| |||||||||||||||||||| |||||||||||| ||||| |||
Db       1628 GAACGGATGATGGCACTGCAGACCGACATTGTGGACCTACAGAGGAGCCCGATGGGTCGG 1687

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              |||||||||| ||  |||| |||||||||
Db       1688 AAGCAGGGGGGCACCTTGGATGACCTAGAG 1717


RESULT 13
US-10-156-610-48
; Sequence 48, Application US/10156610
; Publication No. US20030050270A1
; GENERAL INFORMATION:
;  APPLICANT: Brett P. Monia
;  APPLICANT:  Lex M. Cowsert
;  APPLICANT:  Erich Koller
;  TITLE OF INVENTION: ANTISENSE MODULATION OF INHIBITOR-KAPPA B KINASE-BETA EXPRESSION
;  FILE REFERENCE: ISPH-0666
;  CURRENT APPLICATION NUMBER: US/10/156,610
;  CURRENT FILING DATE:  2002-05-24
;  PRIOR APPLICATION NUMBER: US 09/856,246
;  PRIOR FILING DATE: 2001-08-30
;  PRIOR APPLICATION NUMBER: PCT/US99/16959
;  PRIOR FILING DATE: 1999-07-28
;  PRIOR APPLICATION NUMBER: US 09/197,008
;  PRIOR FILING DATE: 1998-11-20
;  NUMBER OF SEQ ID NOS: 83
; SEQ ID NO 48
;   LENGTH: 2274
;   TYPE: DNA
;   ORGANISM: Mus musculus
US-10-156-610-48

  Query Match             82.2%;  Score 74;  DB 15;  Length 2274;
  Best Local Similarity   88.9%;  Pred. No. 4.6e-16;
  Matches   80;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              || |||||||||||| |||||||| |||||||||||| | |||||||||||| ||||| |||
Db       1603 GAGCGGATGATGGCACTGCAGACTGACATTGTGGACCTGCAGAGGAGCCCGATGGGTCGG 1662

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              |||||||||||  || |||||  |||||||||
Db       1663 AAGCAGGGGGGCACCCTGGATGACCTAGAG 1692


RESULT 14
US-10-087-192-1754
; Sequence 1754, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Engelhard, Eric K.
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
;  TITLE OF INVENTION:  CANCER
;  FILE REFERENCE: 529452000122
;  CURRENT APPLICATION NUMBER: US/10/087,192
;  CURRENT FILING DATE:  2002-03-01
;  PRIOR APPLICATION NUMBER: US 09/747,377
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 2059
```

```
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1754
;    LENGTH: 3210
;    TYPE: DNA
;    ORGANISM: Mus musculus
US-10-087-192-1754

  Query Match             82.2%;  Score 74;  DB 13;  Length 3210;
  Best Local Similarity   88.9%;  Pred. No. 4.6e-16;
  Matches   80;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              || |||||||||||| |||||||| |||||||||||| | |||||||||||| ||||| |||
Db       1647 GAGCGGATGATGGCACTGCAGACTGACATTGTGGACCTGCAGAGGAGCCCGATGGGTCGG 1706

Qy         61 AAGCAGGGGGGAACGCTGGACGACCTAGAG 90
              |||||||||||  ||  |||||  |||||||||
Db       1707 AAGCAGGGGGGCACCCTGGATGACCTAGAG 1736


RESULT 15
US-10-087-192-1753
; Sequence 1753, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Engelhard, Eric K.
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
;  TITLE OF INVENTION:  CANCER
;  FILE REFERENCE: 529452000122
;  CURRENT APPLICATION NUMBER: US/10/087,192
;  CURRENT FILING DATE:  2002-03-01
;  PRIOR APPLICATION NUMBER: US 09/747,377
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 2059
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1753
;    LENGTH: 67076
;    TYPE: DNA
;    ORGANISM: Mus musculus
;    FEATURE:
;    NAME/KEY: misc_feature
;    LOCATION: (1)...(67076)
;    OTHER INFORMATION: n = A,T,C or G
US-10-087-192-1753

  Query Match             77.8%;  Score 70;  DB 13;  Length 67076;
  Best Local Similarity   88.4%;  Pred. No. 1.4e-14;
  Matches   76;  Conservative    0;  Mismatches   10;  Indels    0;  Gaps    0;

Qy          1 GAACGGATGATGGCTCTGCAGACCGACATTGTGGACTTACAGAGGAGCCCCATGGGCCGG 60
              || |||||||||||| |||||||| |||||||||||| | |||||||||||| ||||| |||
Db      48916 GAGCGGATGATGGCACTGCAGACTGACATTGTGGACCTGCAGAGGAGCCCGATGGGTCGG 48975

Qy         61 AAGCAGGGGGGAACGCTGGACGACCT 86
              |||||||||||  ||  |||||  |||||
Db      48976 AAGCAGGGGGGCACCCTGGATGACCT 49001


Search completed: September 24, 2004, 03:50:57
Job time : 383 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 24, 2004, 09:40:54 ; Search time 121 Seconds
(without alignments)
70.053 Million cell updates/sec

Title: US-09-806-701-16_COPY_331_360
Perfect score: 151
Sequence: 1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_29Jan04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	151	100.0	149	4	AAB63781	Aab63781 Human pro
2	151	100.0	552	3	AAY84883	Aay84883 A GFP-I-k
3	151	100.0	750	5	ABB77294	Abb77294 Human IKK
4	151	100.0	756	2	AAW56328	Aaw56328 Inhibitor
5	151	100.0	756	2	AAW49097	Aaw49097 Human I-k
6	151	100.0	756	2	AAW82499	Aaw82499 Human IKK
7	151	100.0	756	2	AAW96158	Aaw96158 Human I k
8	151	100.0	756	2	AAY43247	Aay43247 Human inh
9	151	100.0	756	2	AAW86163	Aaw86163 Human IKK
10	151	100.0	756	2	AAY24051	Aay24051 Human kin
11	151	100.0	756	2	AAW81566	Aaw81566 IkB kinas
12	151	100.0	756	2	AAY14515	Aay14515 Human IKK
13	151	100.0	756	2	AAW81563	Aaw81563 IkB kinas
14	151	100.0	756	5	ABB77306	Abb77306 Human IKK
15	151	100.0	756	5	ABB77296	Abb77296 Human IKK
16	151	100.0	756	5	ABB77295	Abb77295 Human IKK
17	151	100.0	756	5	ABB77300	Abb77300 Human IKK
18	151	100.0	756	5	ABB77293	Abb77293 Human IKK
19	151	100.0	756	5	ABB77304	Abb77304 Human IKK
20	151	100.0	756	5	ABB77298	Abb77298 Human IKK
21	151	100.0	756	5	ABB77302	Abb77302 Human IKK
22	151	100.0	756	5	ABB77297	Abb77297 Human IKK
23	151	100.0	756	5	ABB77308	Abb77308 Human IKK
24	151	100.0	756	5	ABB77307	Abb77307 Human IKK
25	151	100.0	756	5	ABB77299	Abb77299 Human IKK
26	151	100.0	756	5	ABB77301	Abb77301 Human IKK
27	151	100.0	756	5	ABB77305	Abb77305 Human IKK
28	151	100.0	756	5	ABB77310	Abb77310 Human IKK
29	151	100.0	756	5	ABB77303	Abb77303 Human IKK
30	151	100.0	756	5	ABB77309	Abb77309 Human IKK
31	151	100.0	756	6	ABG75804	Abg75804 Human IKK
32	151	100.0	757	6	ABO32508	Abo32508 Human ini
33	151	100.0	1005	3	AAY84882	Aay84882 Amino aci
34	151	100.0	1007	3	AAY84880	Aay84880 Amino aci
35	141	93.4	220	4	AAB94488	Aab94488 Human pro
36	84	55.6	584	3	AAY92057	Aay92057 Murine I
37	84	55.6	745	5	ABB57325	Abb57325 Mouse isc
38	84	55.6	745	6	ABR42682	Abr42682 Mouse IKK
39	79	52.3	745	2	AAW56329	Aaw56329 Inhibitor
40	79	52.3	745	2	AAW82498	Aaw82498 Human IKK
41	79	52.3	745	2	AAW96157	Aaw96157 Human IKK
42	79	52.3	745	2	AAW86164	Aaw86164 Human IKK
43	79	52.3	745	2	AAY24052	Aay24052 Human kin
44	79	52.3	745	2	AAW81565	Aaw81565 IkB kinas
45	79	52.3	745	2	AAY14516	Aay14516 Human IKK

ALIGNMENTS

RESULT 1
AAB63781
ID AAB63781 standard; protein; 149 AA.
XX
AC AAB63781;
XX
DT 26-MAR-2001 (first entry)
XX
DE Human prostate cancer associated antigen protein sequence SEQ ID NO:1143.
XX
KW Human; breast cancer; gastric cancer; prostate cancer; diagnosis;
KW cancer associated antigen; cytostatic; cancer vaccine.
XX
OS Homo sapiens.
XX
PN WO200073801-A2.
XX
PD 07-DEC-2000.
XX
PF 26-MAY-2000; 2000WO-US014749.
XX
PR 28-MAY-1999; 99US-0136526P.
PR 10-SEP-1999; 99US-0153454P.
XX
PA (LUDW-) LUDWIG INST CANCER RES.
XX
PI Obata Y;
XX
DR WPI; 2001-025274/03.
XX
PT Nucleic acids encoding breast, gastric and prostate cancer associated
PT antigen precursors, useful for diagnosing and treating a condition
PT characterized by expression of an abnormal amount of a protein, e.g.
PT cancer.
XX
PS Example 1; Page 715; 799pp; English.
XX
CC AAF22422 to AAF22626, AAF22627 to AAF22773 and AAF22774 to AAF23014
CC represent nucleotide sequences encoding human breast, gastric and
CC prostate cancer associated antigen precursors (CAAP) respectively.
CC AAB63232 to AAB63467, AAB63468 to AAB63721 and AAB63722 to AAB63970
CC represent human breast, gastric and prostate CAAP protein sequence
CC respectively. CAAPs have cytostatic activity and can be used in the
CC production of cancer vaccines. The human CAAP proteins, peptides, nucleic
CC acids or anti-CAAP antibodies are useful for diagnosing and treating a
CC condition characterised by expression of an abnormal amount of a protein,
CC e.g. cancer
XX

```
SQ   Sequence 149 AA;

  Query Match             100.0%;  Score 151;  DB 4;  Length 149;
  Best Local Similarity   100.0%;  Pred. No. 5.7e-15;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ||||||||||||||||||||||||||||||
Db          9 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 38


RESULT 2
AAY84883
ID   AAY84883 standard; protein; 552 AA.
XX
AC   AAY84883;
XX
DT   21-AUG-2000  (first entry)
XX
DE   A GFP-I-kappaB kinase-LZ domain fusion protein.
XX
KW   I-kappaB kinase; cyclic nucleotide phosphodiesterase; cyclic AMP;
KW   cyclic GMP; PDE3; PDE7; PDE8; PDE4 splice variant; PDE4D;
KW   inflammatory disease; chronic inflammation; airway disease; asthma;
KW   chronic bronchial hyper-reactivity; joint disorder; rheumatoid arthritis;
KW   pelvospondylitis; bowel disease; ulcerative colitis; Crohn's disease;
KW   autoimmune disease; diabetes mellitus type I; Hashimoto's thyroiditis;
KW   systemic lupus erythromatosus; myasthenia gravis; Grave's disease;
KW   immune thrombocytopenic purpura; acute respiratory distress syndrome;
KW   septic shock; depression; PDE1; PDE2; PDE6; PDE9; PDE10; jet lag;
KW   PDE5 splice variant; tension; erectile dysfunction; circadian rhythm;
KW   green fluorescent protein; GFP.
XX
OS   Synthetic.
OS   Homo sapiens.
OS   Aequorea victoria.
XX
PN   WO200023091-A2.
XX
PD   27-APR-2000.
XX
PF   15-OCT-1999;   99WO-DK000567.
XX
PR   15-OCT-1998;   98DK-00001321.
PR   15-OCT-1998;   98DK-00001322.
PR   15-OCT-1998;   98DK-00001323.
XX
PA   (BIOI-) BIOIMAGE AS.
XX
PI   Arkhammar POG,  Terry BR,  Scudder KM,  Bjorn SP,  Thastrup O;
XX
DR   WPI; 2000-399281/34.
DR   N-PSDB; AAA14961.
XX
PT   Modulating the activity of I-kappaB kinases or cyclic nucleotide
PT   phosphodiesterases for the treatment of inflammatory disorders,
PT   autoimmune disorders (e.g. diabetes and Crohn's disease) and depression.
XX
PS   Example 3; Page 127-128; 128pp; English.
XX
CC   The specification describes a method for modulating the specific
CC   effectiveness of I-kappaB kinases or cyclic nucleotide phosphodiesterases
CC   which have the ability to cleave cyclic AMP and/or GMP. This involves
CC   modulating the specific effectiveness of the cyclic nucleotide
CC   phosphodiesterase or I-kappaB kinase by modulating the spatial
CC   distribution within cells of the animal. If the cyclic nucleotide
CC   phosphodiesterase used is a PDE3, PDE7, PDE8 or a splice variant of PDE4
CC   (such as PDE4D), the method is used to treat inflammatory diseases such
CC   as chronic inflammation (especially airway diseases such as asthma and
CC   chronic bronchial hyper-reactivity of non-asthma etiology, joint
CC   disorders such as rheumatoid arthritis and pelvospondylitis and bowel
CC   diseases such as ulcerative colitis and Crohn's disease), autoimmune
CC   diseases associated with inflammation (such as diabetes mellitus type I,
CC   systemic lupus erythromatosus, myasthenia gravis, Hashimoto's
CC   thyroiditis, Grave's disease and immune thrombocytopenic purpura),
CC   disregulations of the immune system (such as acute respiratory distress
CC   syndrome (ARDS) and septic shock) and/or depression. Alternatively, if
CC   the cyclic nucleotide phosphodiesterase is PDE1, PDE2, PDE6, PDE9, PDE10
CC   or a splice variant of PDE5, the method is used to treat hypo- or
CC   hypertension, erectile dysfunction, circadian rhythm resetting or jet-
CC   lag. The present sequence represents a fusion protein of green
CC   fluorescent protein (GFP) and I-kappaB kinase and the LZ domain, which is
CC   used in the course of the invention
XX
SQ   Sequence 552 AA;

  Query Match             100.0%;  Score 151;  DB 3;  Length 552;
  Best Local Similarity   100.0%;  Pred. No. 2.5e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ||||||||||||||||||||||||||||||
Db        331 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 360


RESULT 3
ABB77294
ID   ABB77294 standard; protein; 750 AA.
XX
AC   ABB77294;
XX
DT   14-JUN-2002  (first entry)
XX
DE   Human IKKbeta mutant delNBN 737-742.
XX
KW   IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
KW   kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW   autoimmune disease; transplant rejection; osteoporosis; cancer;
KW   Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
KW   rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW   corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
KW   osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;
KW   antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
KW   dermatological; antibacterial; antipsoriatic; antirheumatic;
KW   antiarthritic; osteopathic; antiulcer; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
PN   WO200183547-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US040654.
XX
PR   02-MAY-2000; 2000US-0201261P.
PR   22-AUG-2000; 2000US-00643260.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   May MJ,  Ghosh S;
XX
DR   WPI; 2002-179350/23.
XX
PT   Modulating NF-kappaB induction in a cell, useful for treating e.g.
PT   inflammatory disorders, osteoporosis and cancer, comprises contacting a
PT   cell with an anti-inflammatory compound comprising at least one NEMO
PT   binding domain.
XX
PS   Example 4; Page; 82pp; English.
XX
CC   The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
CC   comprises contacting a cell with an anti-inflammatory compound (ABB08725-
CC   ABB08742) comprising at least one NEMO binding domain (ABB77313). The
CC   compound has acts through selective inhibition of cytokine-mediated NF-kB
CC   activation by blocking the interaction of NEMO with IKKbeta at the NEMO
```

```
CC   binding domain. Blockage of IKKbeta-NEMO interaction results in
CC   inhibition of IKKbeta kinase activation and subsequent decreased
CC   phosphorylation of IkappaB. The compound may also act (directly or
CC   indirectly) by blocking the recruitment of leukocytes into sites of acute
CC   and chronic inflammation, by down-regulating the expression of E-selectin
CC   on leukocytes or by blocking osteoclast differentiation. The compound is
CC   useful in treating NF-kB mediated conditions, where the condition is an
CC   inflammatory disorder, an autoimmune disease, transplant rejection,
CC   osteoporosis, cancer, Alzheimer's disease, atherosclerosis, a viral
CC   infection or ataxia telangiectasia. The inflammatory disorder is asthma,
CC   allergies, urticaria, anaphylaxis, cutaneous inflammation, sepsis,
CC   psoriasis, rheumatoid arthritis, osteoarthritis, psoriatic arthritis,
CC   inflammatory bowel disease, chronic obstructive pulmonary disease,
CC   vasculitis and bursitis. The inflammatory disorder may also be
CC   dermatitis, eczema, psoriasis, osteoarthritis, psoriatic arthritis, lupus
CC   and spondylarthritis. Also for Crohn's disease, ulcerative colitis,
CC   polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
CC   cryoglobulinaemia or multiple sclerosis. For chronic viral infections
CC   caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral
CC   diseases include HIV and influenza. The compound may also be useful for
CC   treating anaphylaxis, drug and food sensitivity, contact dermatitis,
CC   sunburn or aging. The compound may be used to replace corticosteroids in
CC   any application in which corticosteroids are used, including
CC   immunosuppression in transplants and cancer therapy. Also for identifying
CC   antiinflammatory compounds and for diagnosis of an inflammatory disorder.
CC   The compound may be administered alone or in combination with other known
CC   anti-inflammatory agents. The present sequence is that of an IKKbeta
CC   deletion mutant, useful in examples of the invention. Note: The present
CC   sequence is not given in the specification but is derived from GenBank
CC   Accession No. O14920 (ABB77294)
XX
SQ   Sequence 750 AA;

  Query Match             100.0%;  Score 151;  DB 5;  Length 750;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ||||||||||||||||||||||||||||||
Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


RESULT 4
AAW56328
ID   AAW56328 standard; protein; 756 AA.
XX
AC   AAW56328;
XX
DT   24-JUL-1998  (first entry)
XX
DE   Inhibitory subunit I-kappa-B signalsome kinase 2 amino acid sequence.
XX
KW   Inhibitory subunit; I-kappa-B-beta; nuclear factor kappa-B;
KW   NF-kappa-B/Rel dimer; inhibitory activity; phosphorylation;
KW   stimulus-inducible I-kappa-B kinase; IKK; signalsome; I-kappa-B-alpha;
KW   identification; stimulate; signal transduction; the NF-kappa-B cascade;
KW   therapeutic composition; inflammatory; neurodegenerative; disease;
KW   autoimmune disease; cancer.
XX
OS   Homo sapiens.
XX
PN   WO9808955-A1.
XX
PD   05-MAR-1998.
XX
PF   26-AUG-1997;   97WO-US015003.
XX
PR   26-AUG-1996;   96US-00697393.
PR   13-AUG-1997;   97US-00910820.
XX
PA   (SIGN-) SIGNAL PHARM INC.
XX
PI   Mercurio F,  Zhu H,  Barbosa M,  Li G,  Murray BW;
XX
DR   WPI; 1998-179440/16.
DR   N-PSDB; AAV22842.
XX
PT   New isolated stimulus-inducible I-kappa-B kinase signalsome - useful for
PT   developing products for treating, e.g. inflammatory neuro-degenerative
PT   and auto-immune diseases.
XX
PS   Claim 3; Page 60-64; 115pp; English.
XX
CC   The present sequence represents an inhibitory subunit I-kappa-B kinase
CC   (IKK) 2. IKK kinases, when incorporated into an IKK signalsome, are
CC   capable of phosphorylating inhibitory subunit I-kappa-B-alpha, at serine
CC   residues 32 and 36. I-kappa-B-alpha retains nuclear factor (NF) kappa-B
CC   in the cytoplasm. I-kappa-B proteins contain 5-7 ankryin-like repeats
CC   which are required for association with the NF-kappa-B/Rel dimer and for
CC   inhibitory activity. A stimulus-inducible IKK "signalsome" is described
CC   that is capable of specifically phosphorylating I-kappa-B-alpha at
CC   residues S32 and S36, without the addition of exogenous cofactors. The
CC   proteins of the invention can be used to identify agents that inhibit or
CC   stimulate signal transduction via the NF-kappa-B cascade. Therapeutic
CC   compositions comprising such agents may be used for treating a patient
CC   afflicted with a disorder associated with the activation of an IKK
CC   signalsome. The agents may be used to treat, e.g. inflammatory,
CC   neurodegenerative diseases and autoimmune diseases, cancer and viral
CC   infections. The antibodies may be used in a kit for detecting IKK
CC   signalsome activity in a sample
XX
SQ   Sequence 756 AA;

  Query Match             100.0%;  Score 151;  DB 2;  Length 756;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ||||||||||||||||||||||||||||||
Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


RESULT 5
AAW49097
ID   AAW49097 standard; protein; 756 AA.
XX
AC   AAW49097;
XX
DT   07-DEC-1998  (first entry)
XX
DE   Human I-kappa-B kinase (IKK) beta subunit.
XX
KW   I-kappa-B kinase; IKK; human; protein kinase; NF-kappa-B; inflammation;
KW   signal transduction.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Domain          15. .300
FT                   /note= "kinase domain"
FT   Region          458. .486
FT                   /note= "regions contains leucine residues involved in
FT                   leucine zippers"
FT   Domain          602. .642
FT                   /note= "helix-loop-helix domain"
XX
PN   WO9837228-A1.
XX
PD   27-AUG-1998.
XX
PF   23-FEB-1998;   98WO-US003511.
XX
PR   25-FEB-1997;   97US-00810131.
PR   09-OCT-1997;   97US-0061470P.
XX
PA   (REGC ) UNIV CALIFORNIA.
```

XX
PI Karin M, Didonato JA, Rothwarf DM, Hayakawa M, Zandi E;
XX
DR WPI; 1998-467580/40.
DR N-PSDB; AAV32970.
XX
PT Nucleic acid encoding I-kappa-B kinase subunits and antibodies - the sub-
PT units phosphorylate the inhibitor of NF-kappa-B, for studying the
PT inflammatory response and signal transduction pathways.
XX
PS Claim 3; Fig 3; 101pp; English.
XX
CC This is the amino acid sequence of the alpha beta of a human serine
CC protein kinase, designated I-kappa-B kinase (IKK). The IKK beta and alpha
CC (see AAW49096) subunits are cytokine-inducible, share substantial
CC sequence homology, and are activated in response to proinflammatory
CC signals to phosphorylate proteins (I-kappa-Bs) that inhibit the activity
CC of the NF-kappa-B transcription factor. Their amino acid sequences were
CC deduced from cDNA clones (see AAV32969-70). The invention also provides
CC vectors comprising IKK-alpha and -beta nucleic acid molecules, isolated
CC IKK catalytic subunits which can phosphorylate the I-kappa-B protein at
CC Ser-32 and Ser-36, and peptide portions of such IKK subunits. The
CC invention also provides anti-IKK antibodies and their IKK-binding
CC fragments, as well as methods of purifying an IKK complex, methods of
CC identifying an agent which alters the association of an IKK complex or an
CC IKK catalytic subunit with a second protein, and methods of identifying
CC proteins that can interact with an IKK complex or an IKK catalytic
CC subunit. IKK nucleic acids, catalytic subunits and antibodies may be used
CC to study the signal transduction pathways involved in the inflammatory
CC and immune responses, and to identify agents that alter IKK activity,
CC such as protein kinase inhibitors
XX
SQ Sequence 756 AA;

Query Match 100.0%; Score 151; DB 2; Length 756;
Best Local Similarity 100.0%; Pred. No. 3.5e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
||||||||||||||||||||||||||||||
Db 535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564

RESULT 6
AAW82499
ID AAW82499 standard; protein; 756 AA.
XX
AC AAW82499;
XX
DT 04-MAR-1999 (first entry)
XX
DE Human IKK-beta protein.
XX
KW NIK; Nuclear factor-kappa B; NF-kB; signal transduction; TNF; human;
KW tumour necrosis factor; NF-kB-inducing kinase; screening; interaction;
KW modulator; immune response; inflammatory response; viral gene;
KW diagnostic; therapy; IKK-beta.
XX
OS Homo sapiens.
XX
PN US5854003-A.
XX
PD 29-DEC-1998.
XX
PF 26-FEB-1998; 98US-00032475.
XX
PR 03-JUL-1997; 97US-00887518.
XX
PA (TULA-) TULARIK INC.
XX
PI Wu L, Rothe M;
XX
DR WPI; 1999-094902/08.
XX
PT Screening agents for modulating interaction of nuclear factor kappaB
PT inducing kinase - with kinase-binding target, useful for controlling
PT levels of the kinase, for treatment and diagnosis of conditions
PT associated with e.g. inhibition of signal transduction by tumour necrosis
PT factor.
XX
PS Disclosure; Col 23-28; 16pp; English.
XX
CC This sequence represents the human IKK-beta protein, which is used in the
CC isolation of a novel nuclear factor-kappaB (NFkB)-inducing kinase (NIK).
CC This protein is used to screen for agents that modulate the interaction
CC of NIK with a NIK-binding target. The protein can be used as a modulator
CC of cellular functions at the NIK level, or for development of such
CC compounds. NFkB is involved in expression of many immune and inflammatory
CC responses and of some important viral genes. The protein may be used
CC diagnostically and therapeutically, in conditions associated with
CC abnormal utilisation of pathways that involve NFkB, e.g. inhibition of
CC signal transduction by tumour necrosis factor (TNF)
XX
SQ Sequence 756 AA;

Query Match 100.0%; Score 151; DB 2; Length 756;
Best Local Similarity 100.0%; Pred. No. 3.5e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
||||||||||||||||||||||||||||||
Db 535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564

RESULT 7
AAW96158
ID AAW96158 standard; peptide; 756 AA.
XX
AC AAW96158;
XX
DT 27-APR-1999 (first entry)
XX
DE Human I kappa B kinase.
XX
KW I-kappa-B kinase; IKK-alpha; gene expression; modulation; suppression;
KW activation; tumour necrosis factor; TNF; interleukin-1; IL-1;
KW TNF receptor associated factor; TRAF.
XX
OS Homo sapiens.
XX
PN WO9901541-A1.
XX
PD 14-JAN-1999.
XX
PF 01-JUL-1998; 98WO-US013782.
XX
PR 01-JUL-1997; 97US-00887115.
PR 10-JUL-1997; 97US-00890854.
XX
PA (TULA-) TULARIK INC.
XX
PI Rothe M, Cao Z, Regnier C;
XX
DR WPI; 1999-106044/09.
DR N-PSDB; AAX08919.
XX
PT Newly isolated human kinase IkappaB Kinase (IKK-~a) polypeptides - useful
PT in screening for agents that modulate the interaction of an IKK
PT polypeptide to a binding target and for modulating signal transduction
PT involving IkappaB in a cell.
XX
PS Claim 9; Page 21-23; 32pp; English.
XX
CC I-kappa-B, deletion mutants of it retaining I-kappa-B kinase activity and
CC I-kappa-B polypeptides (comprising a six residue domain of I-kappa-B
CC containing one of Ser32 and Ser36, and a candidate agent) can be used to

CC screen for agents that modulate the interaction of an IKK polypeptide to
CC a binding target. The modulation of the kinase activity of IKK-alpha
CC (AAW96157) forms a method for modulating signal transduction involving I-
CC kappa-B in a cell. The IKK-alpha polypeptides are useful for generating
CC oligonucleotide primers and probes for use in the isolation of natural
CC IKK-alpha-encoding nucleic acids. The nucleic acids are useful as
CC translatable transcripts, hybridization probes, polymerase chain reaction
CC (PCR) probes and primers. Their diagnostic applications include IKK-alpha
CC hybridization probes for identifying wild-type and mutant IKK-alpha
CC alleles in clinical and laboratory samples. Therapeutic application
CC includes the use of IKK- alpha nucleic acids for modulating cellular
CC expression or intracellular concentration/availability of active IKK-
CC alpha. Catalytically inactive IKK-alpha mutants suppress NF-kappa-B
CC activation induced by tissue necrosis factor (TNF), interleukin-1 (IL-1)
CC stimulation, TNF receptor-associated factor (TRAF) and NF-kappa-B-
CC inducing kinase (NIK) oversuppression
XX
SQ Sequence 756 AA;

Query Match 100.0%; Score 151; DB 2; Length 756;
Best Local Similarity 100.0%; Pred. No. 3.5e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
||||||||||||||||||||||||||||||
Db 535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564

RESULT 8
AAY43247
ID AAY43247 standard; protein; 756 AA.
XX
AC AAY43247;
XX
DT 13-JAN-2000 (first entry)
XX
DE Human inhibitor-kappa B kinase-beta protein sequence.
XX
KW Inhibitor-kappa B kinase-beta; IKB-beta; human; T-cell leukaemia; asthma;
KW inflammatory response; inflammatory disease; juvenile diabetes mellitus;
KW Graves' disease; rheumatoid arthritis; allograft rejection; diagnosis;
KW inflammatory bowel disease; multiple sclerosis; contact dermatitis;
KW rhinitis; allergy; hyperproliferative disorder; tumour; therapy.
XX
OS Homo sapiens.
XX
PN US5977341-A.
XX
PD 02-NOV-1999.
XX
PF 20-NOV-1998; 98US-00197008.
XX
PR 20-NOV-1998; 98US-00197008.
XX
PA (ISIS-) ISIS PHARM INC.
XX
PI Monia BP, Cowsert LM;
XX
DR WPI; 1999-619715/53.
DR N-PSDB; AAZ31590.
XX
PT Antisense oligonucleotides inhibiting human Inhibitor-kappa B Kinase-
PT beta, useful for treating conditions such as inflammation, asthma,
PT diabetes, allograft rejection, allergies, hyperproliferative disorders or
PT tumors.
XX
PS Claim 1; Col 41-48; 32pp; English.
XX
CC This sequence represents the human inhibitor-kappa B kinase-beta. The
CC invention relates to an antisense oligonucleotide (I) 8 to 30 nucleotides
CC in length inhibiting the expression of human Inhibitor-kappa B kinase-
CC beta (IKB-beta). (I) inhibits the expression of human IKB-beta which
CC plays a role in the development of T-cell leukaemia and in the activation
CC of inflammatory responses. (I) is therefore useful for treating
CC inflammatory diseases or disorders with an inflammatory component such as
CC asthma, juvenile diabetes mellitus, Graves' disease, rheumatoid
CC arthritis, allograft rejection, inflammatory bowel disease, multiple
CC sclerosis, contact dermatitis, rhinitis and various allergies, or
CC hyperproliferative disorders such as leukaemias and other tumours. (I)
CC may also be used for detection of the above disorders
XX
SQ Sequence 756 AA;

Query Match 100.0%; Score 151; DB 2; Length 756;
Best Local Similarity 100.0%; Pred. No. 3.5e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
||||||||||||||||||||||||||||||
Db 535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564

RESULT 9
AAW86163
ID AAW86163 standard; protein; 756 AA.
XX
AC AAW86163;
XX
DT 03-MAR-1999 (first entry)
XX
DE Human IKK-beta polypeptide.
XX
KW IKK-beta; IkappaB kinase; inhibitor; NF-kappaB; nuclear factor-kappaB;
KW nuclear translocation; NF-kappaB-inducing kinase; NIK; recombinant;
KW human.
XX
OS Homo sapiens.
XX
PN US5851812-A.
XX
PD 22-DEC-1998.
XX
PF 10-JUL-1997; 97US-00890853.
XX
PR 01-JUL-1997; 97US-00887114.
XX
PA (TULA-) TULARIK INC.
XX
PI Woronicz J, Goeddel DV;
XX
DR WPI; 1999-080407/07.
DR N-PSDB; AAV84689.
XX
PT DNA encoding IKK-beta polypeptides - useful for producing recombinant
PT polypeptides.
XX
PS Claim 8; Col 13-18; 13pp; English.
XX
CC This represents a IKK-beta (IkappaB kinase) polypeptide. The IkappaB
CC (inhibitor of nuclear factor (NF)-kappaB nuclear translocation) kinase is
CC a NF-kappaB-inducing kinase (NIK)-interacting protein. A host cell
CC containing a recombinant nucleic acid encoding the IKK-beta polypeptide
CC can be used for the recombinant production of the polypeptide
XX
SQ Sequence 756 AA;

Query Match 100.0%; Score 151; DB 2; Length 756;
Best Local Similarity 100.0%; Pred. No. 3.5e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
||||||||||||||||||||||||||||||
Db 535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564

RESULT 10

```
AAY24051
ID   AAY24051 standard; protein; 756 AA.
XX
AC   AAY24051;
XX
DT   20-MAR-2003  (revised)
DT   01-OCT-1999  (first entry)
XX
DE   Human kinase I-kappa-B kinase (IKK-beta).
XX
KW   Nuclear factor kappa-B inducing kinase; NIK; NIK-interacting protein;
KW   human; I-kappa-B kinase; IKK-beta; IKK-beta disorder.
XX
OS   Homo sapiens.
XX
PN   US5939302-A.
XX
PD   17-AUG-1999.
XX
PF   17-JUN-1998;   98US-00099124.
XX
PR   01-JUL-1997;   97US-00887114.
PR   10-JUL-1997;   97US-00890853.
XX
PA   (TULA-) TULARIK INC.
XX
PI   Woronicz J,  Goeddel DV;
XX
DR   WPI; 1999-468406/39.
DR   N-PSDB; AAX98271.
XX
PT   Polypeptides comprising a novel I-kappa-B Kinase useful as hybridization
PT   probes.
XX
PS   Claim 2; Col 13-18; 13pp; English.
XX
CC   The present sequence represents a human I-kappa-B kinase (IKK-beta). The
CC   protein is a nuclear factor kappa-B inducing kinase (NIK) interacting
CC   protein. The IKK-beta nucleic acids, polypeptides, and/or antibodies may
CC   be useful as hybridization primers or probes, translatable transcripts,
CC   diagnostic probes (e.g. for identifying the presence of IKK-beta in a
CC   sample), to detect mutant IKK-beta alleles, in the diagnosis and therapy
CC   of IKK-beta disorders, and in the identification of compounds or agents
CC   that are able to modulate IKK-beta function. (Updated on 20-MAR-2003 to
CC   correct PF field.)
XX
SQ   Sequence 756 AA;

  Query Match             100.0%;  Score 151;  DB 2;  Length 756;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ||||||||||||||||||||||||||||||
Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


RESULT 11
AAW81566
ID   AAW81566 standard; protein; 756 AA.
XX
AC   AAW81566;
XX
DT   04-FEB-1999  (first entry)
XX
DE   IkB kinase (IKK)-beta polpeptide.
XX
KW   NIK; IkB; NF-kB; TNF; kinase; nuclear factor kappa B; inhibition;
KW   tumour necrosis factor; binding; genetic hybridisation; screening;
KW   signal transduction; biopharmaceutical; human.
XX
OS   Homo sapiens.
XX
PN   US5843721-A.
XX
PD   01-DEC-1998.
XX
PF   03-JUL-1997;   97US-00887518.
XX
PR   03-JUL-1997;   97US-00887518.
XX
PA   (TULA-) TULARIK INC.
XX
PI   Wu L,  Rothe M;
XX
DR   WPI; 1999-044580/04.
XX
PT   Probe, vector or recombinant nucleic acid encoding a polypeptide,
PT   especially human nuclear factor kappa-B-inducing kinase protein - useful
PT   for producing recombinant protein.
XX
PS   Example; Col 23-26; 15pp; English.
XX
CC   This represents a IkB kinase (IKK)-alpha polypeptide sequence. The
CC   binding activity of this polypeptide can be activated or inhibited by the
CC   nuclear factor kappa B (NF-kB)-inducing kinase (NIK) polypeptide of the
CC   invention. The NIK polypeptide or its fragment has one or more activities
CC   selected from kinase activity and inhibitory activity; IkB kinase-alpha
CC   and beta binding activity and binding inhibitory activity; tumour
CC   necrosis factor (TNF) receptor-associated factor 2 binding activity and
CC   binding inhibitory activity; IkB binding activity and binding inhibitory
CC   activity, NF-kB activating and inhibitory activity. A vector containing
CC   the NIK nucleic acid can be used to transform host cells for the
CC   recombinant production of the protein. The NIK nucleic acid and the
CC   polypeptide may be used in diagnosis (e.g. genetic hybridisation screen
CC   for NIK transcripts), therapy (e.g. NIK kinase inhibitors to inhibit TNF
CC   signal transduction), and in the biopharmaceutical industry
XX
SQ   Sequence 756 AA;

  Query Match             100.0%;  Score 151;  DB 2;  Length 756;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ||||||||||||||||||||||||||||||
Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


RESULT 12
AAY14515
ID   AAY14515 standard; protein; 756 AA.
XX
AC   AAY14515;
XX
DT   31-AUG-1999  (first entry)
XX
DE   Human IKK-beta protein sequence.
XX
KW   Human; IKK-beta; I-Kappa B-Kinase; inhibitory protein; diagnosis; NF-kB;
KW   Nuclear Factor Kappa B; interaction; binding target.
XX
OS   Homo sapiens.
XX
PN   US5916760-A.
XX
PD   29-JUN-1999.
XX
PF   17-JUN-1998;   98US-00099125.
XX
PR   01-JUL-1997;   97US-00887114.
PR   10-JUL-1997;   97US-00890853.
XX
PA   (TULA-) TULARIK INC.
XX
PI   Goeddel DV,  Woronicz J;
```

XX
DR WPI; 1999-384722/32.
DR N-PSDB; AAX79304.
XX
PT Screening for agents which modulate the interaction of IKK-beta
PT polypeptides and their binding targets.
XX
PS Claim 2; Col 13-18; 14pp; English.
XX
CC This sequence represents human IKK-beta, a novel IkB Kinase (I-Kappa B-
CC Kinase, one of a family of inhibitory proteins which interact with
CC Nuclear Factor Kappa B (NF-kB)). The invention relates to a method of
CC screening for agents which modulate the interaction of human IKK-beta
CC polypeptides and their binding targets. Agents which modulate the IKK-
CC beta binding are useful in a variety of diagnostic and therapeutic
CC applications where the disease is associated with improper utilization of
CC a pathway involving IKK-beta proteins (e.g. NF-kB activation and IKK-beta
CC -dependent transcriptional activation)
XX
SQ Sequence 756 AA;

Query Match 100.0%; Score 151; DB 2; Length 756;
Best Local Similarity 100.0%; Pred. No. 3.5e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
||||||||||||||||||||||||||||||
Db 535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564

RESULT 13
AAW81563
ID AAW81563 standard; protein; 756 AA.
XX
AC AAW81563;
XX
DT 04-FEB-1999 (first entry)
XX
DE IkB kinase (IKK)-beta polpeptide.
XX
KW NIK; IkB; NF-kB; TNF; kinase; nuclear factor kappa B; inhibition;
KW tumour necrosis factor; binding; genetic hybridisation; screening;
KW signal transduction; biopharmaceutical; immunogen; pharmacological;
KW transcription regulator; human.
XX
OS Homo sapiens.
XX
PN US5844073-A.
XX
PD 01-DEC-1998.
XX
PF 13-FEB-1998; 98US-00023321.
XX
PR 03-JUL-1997; 97US-00887518.
XX
PA (TULA-) TULARIK INC.
XX
PI Wu L, Rothe M;
XX
DR WPI; 1999-044664/04.
XX
PT New isolated peptide comprising a specified 947 amino acid sequence - has
PT e.g. kinase activity, kinase inhibitory activity, IkB kinase-alpha
PT binding activity, and IkB kinase-alpha binding inhibitory activity.
XX
PS Example; Col 23-26; 15pp; English.
XX
CC This represents a IkB kinase (IKK)-beta polypeptide sequence. The binding
CC activity of this polypeptide can be activated or inhibited by the nuclear
CC factor kappa B (NF-kB)-inducing kinase (NIK) polypeptide of the
CC invention. The NIK polypeptide or its fragment has one or more activities
CC selected from kinase activity and inhibitory activity; IkB kinase-alpha
CC and beta binding activity and binding inhibitory activity; tumour
CC necrosis factor (TNF) receptor-associated factor 2 binding activity and
CC binding inhibitory activity; IkB binding activity and binding inhibitory
CC activity, NF-kB activating and inhibitory activity. The NIK nucleic acid
CC and the polypeptide may be used in diagnosis (e.g. genetic hybridisation
CC screen for NIK transcripts), therapy (e.g. NIK kinase inhibitors to
CC inhibit TNF signal transduction), and in the biopharmaceutical industry
CC (e.g. as immunogens, reagents for isolating other transcription
CC regulators, and reagents for screening chemical libraries for
CC pharmacological agents)
XX
SQ Sequence 756 AA;

Query Match 100.0%; Score 151; DB 2; Length 756;
Best Local Similarity 100.0%; Pred. No. 3.5e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
||||||||||||||||||||||||||||||
Db 535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564

RESULT 14
ABB77306
ID ABB77306 standard; protein; 756 AA.
XX
AC ABB77306;
XX
DT 14-JUN-2002 (first entry)
XX
DE Human IKKbeta mutant S740A.
XX
KW IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
KW kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW autoimmune disease; transplant rejection; osteoporosis; cancer;
KW Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
KW rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
KW osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;
KW antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
KW dermatological; antibacterial; antipsoriatic; antirheumatic;
KW antiarthritic; osteopathic; antiulcer; mutant; mutein.
XX
OS Homo sapiens.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 740
FT /note= "Wildtype Ser substituted by Ala"
XX
PN WO200183547-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001WO-US040654.
XX
PR 02-MAY-2000; 2000US-0201261P.
PR 22-AUG-2000; 2000US-00643260.
XX
PA (UYYA) UNIV YALE.
XX
PI May MJ, Ghosh S;
XX
DR WPI; 2002-179350/23.
XX
PT Modulating NF-kappaB induction in a cell, useful for treating e.g.
PT inflammatory disorders, osteoporosis and cancer, comprises contacting a
PT cell with an anti-inflammatory compound comprising at least one NEMO
PT binding domain.
XX
PS Example 11; Page; 82pp; English.
XX
CC The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
CC comprises contacting a cell with an anti-inflammatory compound (ABB08725-

```
CC   ABB08742) comprising at least one NEMO binding domain (ABB77313). The
CC   compound has acts through selective inhibition of cytokine-mediated NF-kB
CC   activation by blocking the interaction of NEMO with IKKbeta at the NEMO
CC   binding domain. Blockage of IKKbeta-NEMO interaction results in
CC   inhibition of IKKbeta kinase activation and subsequent decreased
CC   phosphorylation of IkappaB. The compound may also act (directly or
CC   indirectly) by blocking the recruitment of leukocytes into sites of acute
CC   and chronic inflammation, by down-regulating the expression of E-selectin
CC   on leukocytes or by blocking osteoclast differentiation. The compound is
CC   useful in treating NF-kB mediated conditions, where the condition is an
CC   inflammatory disorder, an autoimmune disease, transplant rejection,
CC   osteoporosis, cancer, Alzheimer's disease, atherosclerosis, a viral
CC   infection or ataxia telangiectasia. The inflammatory disorder is asthma,
CC   allergies, urticaria, anaphylaxis, cutaneous inflammation, sepsis,
CC   psoriasis, rheumatoid arthritis, osteoarthritis, psoriatic arthritis,
CC   inflammatory bowel disease, chronic obstructive pulmonary disease,
CC   vasculitis and bursitis. The inflammatory disorder may also be
CC   dermatitis, eczema, psoriasis, osteoarthritis, psoriatic arthritis, lupus
CC   and spondylarthritis. Also for Crohn's disease, ulcerative colitis,
CC   polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
CC   cryoglobulinaemia or multiple sclerosis. For chronic viral infections as
CC   caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral
CC   diseases include HIV and influenza. The compound may also be useful for
CC   treating anaphylaxis, drug and food sensitivity, contact dermatitis,
CC   sunburn or aging. The compound may be used to replace corticosteroids in
CC   any application in which corticosteroids are used, including
CC   immunosuppression in transplants and cancer therapy. Also for identifying
CC   antiinflammatory compounds and for diagnosis of an inflammatory disorder.
CC   The compound may be administered alone or in combination with other known
CC   anti-inflammatory agents. The present sequence is that of an IKKbeta
CC   mutant, useful in examples of the invention. Note: The present sequence
CC   is not given in the specification but is derived from GenBank Accession
CC   No. O14920 (ABB77294)
XX
SQ   Sequence 756 AA;

  Query Match             100.0%;  Score 151;  DB 5;  Length 756;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ||||||||||||||||||||||||||||||
Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


RESULT 15
ABB77296
ID   ABB77296 standard; protein; 756 AA.
XX
AC   ABB77296;
XX
DT   14-JUN-2002  (first entry)
XX
DE   Human IKKbeta mutant W739F.
XX
KW   IKKbeat; IKKalpha; NEMO; NEMO binding domain; NBD; NF-kappaB; NF-kB;
KW   kinase activation; leukocyte; inflammation; E-selectin; osteoclast;
KW   autoimmune disease; transplant rejection; osteoporosis; cancer;
KW   Alzheimer's disease; viral; infection; asthma; anaphylaxis; psoriasis;
KW   rheumatoid arthritis; Crohn's disease; multiple sclerosis; HIV;
KW   corticosteroid; immunosuppression; antiinflammatory; immunosuppressive;
KW   osteopathic; cytostatic; nootropic; neuroprotective; anti-HIV; human;
KW   antiarteriosclerotic; virucide; antiasthmatic; antiallergic;
KW   dermatological; antibacterial; antipsoriatic; antirheumatic;
KW   antiarthritic; osteopathic; antiulcer; mutant; mutein.
XX
OS   Homo sapiens.
OS   Synthetic.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 739
FT                   /note= "Wildtype Trp substituted by Phe"
XX
PN   WO200183547-A2.
XX
PD   08-NOV-2001.
XX
PF   02-MAY-2001; 2001WO-US040654.
XX
PR   02-MAY-2000; 2000US-0201261P.
PR   22-AUG-2000; 2000US-00643260.
XX
PA   (UYYA ) UNIV YALE.
XX
PI   May MJ,  Ghosh S;
XX
DR   WPI; 2002-179350/23.
XX
PT   Modulating NF-kappaB induction in a cell, useful for treating e.g.
PT   inflammatory disorders, osteoporosis and cancer, comprises contacting a
PT   cell with an anti-inflammatory compound comprising at least one NEMO
PT   binding domain.
XX
PS   Example 11; Page; 82pp; English.
XX
CC   The invention relates to modulating NF-kappaB (NF-kB) induction in a cell
CC   comprises contacting a cell with an anti-inflammatory compound (ABB08725-
CC   ABB08742) comprising at least one NEMO binding domain (ABB77313). The
CC   compound has acts through selective inhibition of cytokine-mediated NF-kB
CC   activation by blocking the interaction of NEMO with IKKbeta at the NEMO
CC   binding domain. Blockage of IKKbeta-NEMO interaction results in
CC   inhibition of IKKbeta kinase activation and subsequent decreased
CC   phosphorylation of IkappaB. The compound may also act (directly or
CC   indirectly) by blocking the recruitment of leukocytes into sites of acute
CC   and chronic inflammation, by down-regulating the expression of E-selectin
CC   on leukocytes or by blocking osteoclast differentiation. The compound is
CC   useful in treating NF-kB mediated conditions, where the condition is an
CC   inflammatory disorder, an autoimmune disease, transplant rejection,
CC   osteoporosis, cancer, Alzheimer's disease, atherosclerosis, a viral
CC   infection or ataxia telangiectasia. The inflammatory disorder is asthma,
CC   allergies, urticaria, anaphylaxis, cutaneous inflammation, sepsis,
CC   psoriasis, rheumatoid arthritis, osteoarthritis, psoriatic arthritis,
CC   inflammatory bowel disease, chronic obstructive pulmonary disease,
CC   vasculitis and bursitis. The inflammatory disorder may also be
CC   dermatitis, eczema, psoriasis, osteoarthritis, psoriatic arthritis, lupus
CC   and spondylarthritis. Also for Crohn's disease, ulcerative colitis,
CC   polymyalgia, scleroderma, Wegner's granulomatosis, temporal arteritis,
CC   cryoglobulinaemia or multiple sclerosis. For chronic viral infections
CC   caused by Epstein-barr, cytomegalovirus or herpes simplex. Other viral
CC   diseases include HIV and influenza. The compound may also be useful for
CC   treating anaphylaxis, drug and food sensitivity, contact dermatitis,
CC   sunburn or aging. The compound may be used to replace corticosteroids in
CC   any application in which corticosteroids are used, including
CC   immunosuppression in transplants and cancer therapy. Also for identifying
CC   antiinflammatory compounds and for diagnosis of an inflammatory disorder.
CC   The compound may be administered alone or in combination with other known
CC   anti-inflammatory agents. The present sequence is that of an IKKbeta
CC   mutant, useful in examples of the invention. Note: The present sequence
CC   is not given in the specification but is derived from GenBank Accession
CC   No. O14920 (ABB77294)
XX
SQ   Sequence 756 AA;

  Query Match             100.0%;  Score 151;  DB 5;  Length 756;
  Best Local Similarity   100.0%;  Pred. No. 3.5e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ||||||||||||||||||||||||||||||
Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


Search completed: September 24, 2004, 09:43:05
Job time : 123 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 24, 2004, 09:40:59 ; Search time 38 Seconds
(without alignments)
75.941 Million cell updates/sec

Title: US-09-806-701-16_COPY_331_360
Perfect score: 151
Sequence: 1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_78:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	84	55.6	745	1	I49101	conserved helix-lo
2	55	36.4	283	2	H83026	chemotaxis protein
3	54	35.8	387	1	XUEC	acetyl-CoA C-acylt
4	54	35.8	387	2	E91225	acetyl-CoA transfe
5	54	35.8	387	2	C86072	acetyl-CoA transfe
6	54	35.8	387	2	AI0914	small (beta) chain
7	54	35.8	391	1	JS0624	fatty-acid beta-ox
8	54	35.8	391	2	F83269	fatty-acid oxidati
9	53	35.1	387	2	A82036	fatty oxidation co
10	52.5	34.8	649	2	C90113	glucose inhibited
11	52	34.4	387	2	AG0458	acetyl-CoA C-acylt
12	51	33.8	237	2	JQ0729	60K inner-membrane
13	49.5	32.8	297	2	C83776	oxidoreductase BH1
14	49	32.5	890	2	E86530	initiation factor-
15	49	32.5	890	2	E81576	translation initia
16	49	32.5	890	2	F72093	translation initia
17	49	32.5	892	2	H71558	probable translati
18	49	32.5	896	2	G81709	translation initia
19	48.5	32.1	373	2	A83341	glycine cleavage s
20	48	31.8	325	2	B95980	probable C4-dicarb
21	48	31.8	400	2	T47111	probable acetyl-Co
22	48	31.8	539	2	S43060	CCT (chaperonin co
23	48	31.8	601	2	S74239	secretogranin II p
24	48	31.8	1627	2	AE2109	two-component hybr
25	47.5	31.5	402	2	T20595	hypothetical prote
26	47	31.1	436	2	T15331	hypothetical prote
27	47	31.1	454	2	T45260	hypothetical prote
28	47	31.1	466	2	G87612	cytosol aminopepti
29	47	31.1	489	2	AE2810	glycerol kinase 2
30	47	31.1	489	2	H97588	glycerol kinase 2
31	47	31.1	528	2	S67690	chaperonin CCT4, c
32	46	30.5	325	2	D70903	hypothetical prote
33	46	30.5	360	2	F96902	aspartate-semialde
34	46	30.5	610	2	AE1472	two-component sens
35	46	30.5	610	2	AI1110	two-component sens
36	46	30.5	955	2	T00247	zinc finger protei
37	46	30.5	1062	2	D96540	hypothetical prote
38	46	30.5	1561	2	T00248	zinc finger protei
39	45.5	30.1	387	2	E82777	phage-related inte
40	45.5	30.1	389	2	AD1614	Acetyl-CoA acetylt
41	45.5	30.1	389	2	AF1251	Acetyl-CoA acetylt
42	45.5	30.1	405	2	H70893	probable beta-keto
43	45	29.8	281	2	S69525	hypothetical prote
44	45	29.8	306	2	T21385	hypothetical prote
45	45	29.8	318	2	T49714	related to spliceo

ALIGNMENTS

RESULT 1
I49101
conserved helix-loop-helix ubiquitous kinase (EC 2.7.1.-) CHUK - mouse
C;Species: Mus musculus (house mouse)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C;Accession: I49101
R;Mock, B.A.; Connelly, M.A.; McBride, O.W.; Kozak, C.A.; Marcu, K.B.
Genomics 27, 348-351, 1995
A;Title: CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human chromosome 1
A;Reference number: I49101; MUID:96044444; PMID:7558004
A;Accession: I49101
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-745 <RES>
A;Cross-references: EMBL:U12473; NID:g1079492; PIDN:AAC52589.1; PID:g1079493
C;Genetics:
A;Gene: CHUK
C;Superfamily: mouse conserved helix-loop-helix ubiquitous kinase; protein kinase homolog
C;Keywords: ATP; phosphotransferase
F;13-283/Domain: protein kinase homology <KIN>

Query Match 55.6%; Score 84; DB 1; Length 745;
Best Local Similarity 46.7%; Pred. No. 0.00012;
Matches 14; Conservative 11; Mismatches 5; Indels 0; Gaps 0;

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Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              :::|:| |:|::||:|| ||:||  :: ||
Db        532 DQIMSLHTEIMELQKSPYGRRQGDLMESLE 561
```

RESULT 2
H83026
chemotaxis protein MotA PA4954 [imported] - Pseudomonas aeruginosa (strain PAO1)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: H83026
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83026
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-283 <STO>
A;Cross-references: GB:AE004908; GB:AE004091; NID:g9951230; PIDN:AAG08339.1; GSPDB:GN001
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: motA; PA4954
C;Superfamily: motA protein

```
  Query Match             36.4%;  Score 55;  DB 2;  Length 283;
  Best Local Similarity   46.4%;  Pred. No. 1.2;
  Matches   13;  Conservative    3;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDD 28
              | |||:: || |   ||:  |  | | |
Db         91 EGMMAIEADIEDPAASPIFSKYPGVLKD 118


RESULT 3
XUEC
acetyl-CoA C-acyltransferase (EC 2.3.1.16) - Escherichia coli (strain K-12)
N;Alternate names: 3-ketoacyl-CoA thiolase; beta-ketothiolase; degradative thiolase; fat
C;Species: Escherichia coli
C;Date: 30-Jun-1991 #sequence_revision 10-Oct-1997 #text_change 01-Mar-2002
C;Accession: F65189; JV0109; JQ0655; A35436; S30736; A40816
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A;Title: The complete genome sequence of Escherichia coli K-12.
A;Reference number: A64720; MUID:97426617; PMID:9278503
A;Accession: F65189
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-387 <BLAT>
A;Cross-references: GB:AE000460; GB:U00096; NID:g2367315; PIDN:AAC76848.1; PID:g2367316;
A;Experimental source: strain K-12, substrain MG1655
R;Dirusso, C.C.
J. Bacteriol. 172, 6459-6468, 1990
A;Title: Primary sequence of the Escherichia coli fadBA operon, encoding the fatty acid-
A;Reference number: JV0108; MUID:91035260; PMID:1699931
A;Accession: JV0109
A;Molecule type: DNA
A;Residues: 1-36,'S',38-387 <DIR>
A;Cross-references: GB:M59368; GB:M36149; NID:g145899; PIDN:AAA23751.1; PID:g145901
R;Nakahigashi, K.; Inokuchi, H.
Nucleic Acids Res. 18, 4937, 1990
A;Title: Nucleotide sequence of the fadA and fadB genes from Escherichia coli.
A;Reference number: JQ0654; MUID:90370500; PMID:2204034
A;Accession: JQ0655
A;Molecule type: DNA
A;Residues: 1-118,'G',120-387 <NAK>
A;Cross-references: EMBL:X52837; NID:g41370; PIDN:CAB40810.1; PID:g4584723
R;Yang, S.Y.; Yang, X.Y.H.; Healy-Louie, G.; Schulz, H.; Elzinga, M.
J. Biol. Chem. 265, 10424-10429, 1990
A;Title: Nucleotide sequence of the fadA gene. Primary structure of 3-ketoacyl-coenzyme
A;Reference number: A35436; MUID:90285166; PMID:2191949
A;Accession: A35436
A;Molecule type: DNA
A;Residues: 1-36,'S',38-370,'DG',373,'VS',375-387 <YAN>
A;Cross-references: EMBL:J05498
R;Daniels, D.L.; Plunkett III, G.; Burland, V.; Blattner, F.R.
Science 257, 771-778, 1992
A;Title: Analysis of the Escherichia coli genome: DNA sequence of the region from 84.5 t
A;Reference number: S30660; MUID:92358234; PMID:1379743
A;Accession: S30736
A;Molecule type: DNA
A;Residues: 1-48,'X',50-81,'X',83-170,'XX',173-339,'X',341-387 <DAN>
A;Cross-references: EMBL:M87049
R;Yang, S.Y.; Yang, X.Y.H.; Healy-Louie, G.; Schulz, H.; Elzinga, M.
J. Biol. Chem. 266, 16255, 1991
A;Reference number: A40816; MUID:91340783; PMID:1678742
A;Contents: erratum
A;Accession: A40816
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 368-377 <YA2>
C;Genetics:
A;Gene: fadA
A;Map position: 87 min
C;Function:
A;Description: catalyzes the transfer of the acyl group from acyl-CoA to acetyl-CoA to f
A;Pathway: fatty acid beta-oxidation
A;Note: the E. coli enzyme is the beta chain of the fatty acid complex
C;Superfamily: acetyl-CoA acetyltransferase
C;Keywords: acyltransferase; coenzyme A; fatty acid beta-oxidation
F;91/Active site: Cys #status predicted

  Query Match             35.8%;  Score 54;  DB 1;  Length 387;
  Best Local Similarity   61.1%;  Pred. No. 2.4;
  Matches   11;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          7 QTDIVDLQRSPMGRKQGG 24
              |  |||  |:|||| :||
Db          3 QVVIVDAIRTPMGRSKGG 20


RESULT 4
E91225
acetyl-CoA transferase [imported] - Escherichia coli (strain O157:H7, substrain RIMD 050
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C;Accession: E91225
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
A;Reference number: A99629; MUID:21156231; PMID:11258796
A;Accession: E91225
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-387 <HAY>
A;Cross-references: GB:BA000007; PIDN:BAB38196.1; PID:g13364249; GSPDB:GN00154
A;Experimental source: strain O157:H7, substrain RIMD 0509952
C;Genetics:
A;Gene: ECs4773
C;Superfamily: acetyl-CoA acetyltransferase

  Query Match             35.8%;  Score 54;  DB 2;  Length 387;
  Best Local Similarity   61.1%;  Pred. No. 2.4;
  Matches   11;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          7 QTDIVDLQRSPMGRKQGG 24
              |  |||  |:|||| :||
Db          3 QVVIVDAIRTPMGRSKGG 20


RESULT 5
C86072
acetyl-CoA transferase [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 27-Nov-2001
C;Accession: C86072
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: C86072
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-387 <STO>
A;Cross-references: GB:AE005174; NID:g12518723; PIDN:AAG59039.1; GSPDB:GN00145; UWGP:Z53
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: fadA
C;Superfamily: acetyl-CoA acetyltransferase

  Query Match             35.8%;  Score 54;  DB 2;  Length 387;
  Best Local Similarity   61.1%;  Pred. No. 2.4;
  Matches   11;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          7 QTDIVDLQRSPMGRKQGG 24
              |  |||  |:|||| :||
Db          3 QVVIVDAIRTPMGRSKGG 20
```

RESULT 6
AI0914
small (beta) chain of the fatty acid-oxidizing multienzyme complex [imported] - Salmonel
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AI0914
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
, S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AI0914
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-387 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD07911.1; PID:g16504456; GSPDB:GN00176
C;Genetics:
A;Gene: STY3578
C;Superfamily: acetyl-CoA acetyltransferase

  Query Match 35.8%; Score 54; DB 2; Length 387;
  Best Local Similarity 61.1%; Pred. No. 2.4;
  Matches 11; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 7 QTDIVDLQRSPMGRKQGG 24
| ||| |:|||| :||
Db 3 QVVIVDAIRTPMGRSKGG 20

RESULT 7
JS0624
fatty-acid beta-oxidation multienzyme complex beta chain - Pseudomonas fragi
N;Alternate names: acetyl-CoA C-acyltransferase homolog
N;Contains: acetyl-CoA C-acyltransferase (EC 2.3.1.16)
C;Species: Pseudomonas fragi
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C;Accession: JS0624; PS0268
R;Sato, S.; Hayashi, M.; Imamura, S.; Ozeki, Y.; Kawaguchi, A.
J. Biochem. 111, 8-15, 1992
A;Title: Primary structures of the genes, faoA and faoB, from Pseudomonas fragi B-0771 w
A;Reference number: JX0199; MUID:92299657; PMID:1607366
A;Accession: JS0624
A;Molecule type: DNA
A;Residues: 1-391 <SAT>
A;Cross-references: GB:D10390; GB:D90447; NID:g391838; PIDN:BAA01228.1; PID:g391840
A;Experimental source: strain B-0771
A;Accession: PS0268
A;Molecule type: protein
A;Residues: 20-41;161-182;207-229;262-294;298-320;336-350,'X',352-353 <SAT1>
C;Genetics:
A;Gene: faoB
C;Complex: heterotetramer of 2 alpha and 2 beta chains
C;Function:
A;Description: catalyzes the cleavage of a 3-ketoacyl-coenzyme A by coenzyme A to acetyl
A;Pathway: fatty acid beta-oxidation
C;Superfamily: acetyl-CoA acetyltransferase
C;Keywords: acyltransferase; coenzyme A; fatty acid beta-oxidation; heterotetramer
F;2-391/Product: fatty-acid beta-oxidation multienzyme complex beta chain #status predic

  Query Match 35.8%; Score 54; DB 1; Length 391;
  Best Local Similarity 66.7%; Pred. No. 2.4;
  Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 10 IVDLQRSPMGRKQGG 24
||| |:|||| :||
Db 10 IVDFGRTPMGRSKGG 24

RESULT 8
F83269
fatty-acid oxidation complex beta-subunit PA3013 [imported] - Pseudomonas aeruginosa (st
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C;Accession: F83269
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, M.J.; Bri
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: F83269
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-391 <STO>
A;Cross-references: GB:AE004726; GB:AE004091; NID:g9949108; PIDN:AAG06401.1; GSPDB:GN0013
A;Experimental source: strain PAO1
C;Genetics:
A;Gene: foaB; PA3013
C;Superfamily: acetyl-CoA acetyltransferase

  Query Match 35.8%; Score 54; DB 2; Length 391;
  Best Local Similarity 66.7%; Pred. No. 2.4;
  Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 10 IVDLQRSPMGRKQGG 24
||| |:|||| :||
Db 10 IVDFGRTPMGRSKGG 24

RESULT 9
A82036
fatty oxidation complex, beta chain VC2759 [imported] - Vibrio cholerae (strain N16961 se
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: A82036
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.
l, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: A82036
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-387 <HEI>
A;Cross-references: GB:AE004342; GB:AE003852; NID:g9657358; PIDN:AAF95898.1; GSPDB:GN0012
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC2759
A;Map position: 1
C;Superfamily: acetyl-CoA acetyltransferase

  Query Match 35.1%; Score 53; DB 2; Length 387;
  Best Local Similarity 66.7%; Pred. No. 3.4;
  Matches 10; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 10 IVDLQRSPMGRKQGG 24
||| |:|||| :||
Db 6 IVDCLRTPMGRSKGG 20

RESULT 10
C90113
glucose inhibited division protein A [imported] - Guillardia theta nucleomorph
C;Species: nucleomorph Guillardia theta
A;Note: a nucleomorph is the vestigial nucleus of a eukaryotic endosymbiont
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 15-Jun-2001
C;Accession: C90113
R;Douglas, S.; Zauner, S.; Fraunholz, M.; Beaton, M.; Penny, S.; Deng, L.T.; Wu, X.; Reit
Nature 410, 1091-1096, 2001
A;Title: The highly reduced genome of an enslaved algal nucleus.
A;Reference number: A99082; MUID:11323671; PMID:11323671

```
A;Accession: C90113
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-649 <DOU>
A;Cross-references: GB:AJ010592; NID:g12580753; PIDN:CAC27071.1; GSPDB:GN00151
C;Genetics:
A;Gene: putative N-terminal transit sequence
A;Map position: 2
A;Genome: nucleomorph
C;Superfamily: gidA protein
C;Keywords: nucleomorph

  Query Match             34.8%;  Score 52.5;  DB 2;  Length 649;
  Best Local Similarity   41.4%;  Pred. No. 7.1;
  Matches   12;  Conservative    6;  Mismatches   10;  Indels    1;  Gaps    1;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDL 29
              |  | |: |  |::  |:|||  | :||:
Db        459 EYRMLLRGDNADIRLKPLGRKY-GLVDDI 486


RESULT 11
AG0458
acetyl-CoA C-acyltransferase (EC 2.3.1.16) [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
C;Accession: AG0458
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AG0458
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-387 <KUR>
A;Cross-references: GB:AL590842; PIDN:CAC93235.1; PID:g15981682; GSPDB:GN00175
C;Genetics:
A;Gene: fadA
C;Superfamily: acetyl-CoA acetyltransferase
C;Keywords: acyltransferase; coenzyme A

  Query Match             34.4%;  Score 52;  DB 2;  Length 387;
  Best Local Similarity   60.0%;  Pred. No. 4.8;
  Matches    9;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 IVDLQRSPMGRKQGG 24
              |:|  |:|||| :||
Db          6 IIDAVRTPMGRSKGG 20


RESULT 12
JQ0729
60K inner-membrane protein - Proteus mirabilis (fragment)
C;Species: Proteus mirabilis
C;Date: 12-Mar-1993 #sequence_revision 12-Mar-1993 #text_change 08-Oct-1999
C;Accession: JQ0729
R;Skovgaard, O.
Gene 93, 27-34, 1990
A;Title: Nucleotide sequence of a Proteus mirabilis DNA fragment homologous to the 60K-r
A;Reference number: JQ0729; MUID:91033012; PMID:2172087
A;Accession: JQ0729
A;Molecule type: DNA
A;Residues: 1-237 <SKO>
A;Cross-references: GB:M58352; GB:M31295; NID:g150873; PIDN:AAA83954.1; PID:g150874
A;Experimental source: strain LM1509
C;Keywords: DNA replication; membrane protein

  Query Match             33.8%;  Score 51;  DB 2;  Length 237;
  Best Local Similarity   31.0%;  Pred. No. 4;
  Matches    9;  Conservative   12;  Mismatches    4;  Indels    4;  Gaps    1;

Qy          2 RMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ::: ::||::||: :     ||||:|: :
Db         61 KLITVKTDVLDLRIN----TQGGTIDEAD 85


RESULT 13
C83776
oxidoreductase BH1011 [imported] - Bacillus halodurans (strain C-125)
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
C;Accession: C83776
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83776
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-297 <STO>
A;Cross-references: GB:AP001510; GB:BA000004; NID:g10173440; PIDN:BAB04730.1; GSPDB:GN00
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH1011
C;Superfamily: fission yeast pyridoxine 4-dehydrogenase

  Query Match             32.8%;  Score 49.5;  DB 2;  Length 297;
  Best Local Similarity   39.3%;  Pred. No. 8.7;
  Matches   11;  Conservative    5;  Mismatches    7;  Indels    5;  Gaps    1;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDD 28
              : :  |||| :||      :  |||:||
Db        103 DSLRRLQTDYIDLY-----QLHGGTIDD 125


RESULT 14
E86530
initiation factor-2 [imported] - Chlamydophila pneumoniae (strain J138)
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-2001
C;Accession: E86530
R;Shirai, M.; Hirakawa, H.; Kimoto, M.; Tabuchi, M.; Kishi, F.; Ouchi, K.; Shiba, T.; Is
Nucleic Acids Res. 28, 2311-2314, 2000
A;Title: Comparison of whole genome sequences of chlamydia pneumoniae J138.
A;Reference number: A86491; MUID:20330349; PMID:10871362
A;Accession: E86530
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-890 <STO>
A;Cross-references: GB:BA000008; NID:g8978691; PIDN:BAA98527.1; GSPDB:GN00142
A;Experimental source: strain J138
C;Genetics:
A;Gene: infB
C;Superfamily: translation initiation factor IF-2; translation elongation factor Tu homo

  Query Match             32.5%;  Score 49;  DB 2;  Length 890;
  Best Local Similarity   38.1%;  Pred. No. 34;
  Matches    8;  Conservative    7;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          3 MMALQTDIVDLQRSPMGRKQG 23
              |:||| :::|:  |  | :|
Db        553 MLALQAEVLELKADPSARARG 573


RESULT 15
E81576
translation initiation factor 2 CP0440 [imported] - Chlamydophila pneumoniae (strain AR39
C;Species: Chlamydophila pneumoniae, Chlamydia pneumoniae
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 21-Jul-2000
C;Accession: E81576
R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, E
, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg,
Nucleic Acids Res. 28, 1397-1406, 2000
A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39.
```

A;Reference number: A81500; MUID:20150255; PMID:10684935
A;Accession: E81576
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-890 <REA>
A;Cross-references: GB:AE002205; GB:AE002161; NID:g7189360; PIDN:AAF38279.1; PID:g718936
A;Experimental source: strain AR39, HL cells
C;Genetics:
A;Gene: CP0440
C;Superfamily: translation initiation factor IF-2; translation elongation factor Tu homo

Query Match 32.5%; Score 49; DB 2; Length 890;
Best Local Similarity 38.1%; Pred. No. 34;
Matches 8; Conservative 7; Mismatches 6; Indels 0; Gaps 0;

```
Qy          3 MMALQTDIVDLQRSPMGRKQG 23
              |:||| :::::|:  |  | :|
Db        553 MLALQAEVLELKADPSARARG 573
```

Search completed: September 24, 2004, 09:46:21
Job time : 40 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 24, 2004, 09:40:54 ; Search time 23 Seconds
(without alignments)
67.918 Million cell updates/sec

Title: US-09-806-701-16_COPY_331_360
Perfect score: 151
Sequence: 1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	151	100.0	756	1	IKKB_HUMAN	O14920 homo sapien
2	151	100.0	757	1	IKKB_MOUSE	O88351 mus musculu
3	151	100.0	757	1	IKKB_RAT	Q9qy78 rattus norv
4	84	55.6	745	1	IKKA_MOUSE	Q60680 m inhibitor
5	79	52.3	745	1	IKKA_HUMAN	O15111 h inhibitor
6	54	35.8	387	1	THIK_ECO57	Q8x8j4 escherichia
7	54	35.8	387	1	THIK_ECOLI	P21151 escherichia
8	54	35.8	387	1	THIK_SALTY	Q9l616 salmonella
9	54	35.8	390	1	THIK_PSEFR	P28790 pseudomonas
10	52	34.4	387	1	THIK_YERPE	Q8zam9 yersinia pe
11	51	33.8	237	1	OXAA_PROMI	P22833 proteus mir
12	51	33.8	656	1	ACSA_SYNEL	Q8dkh2 synechococc
13	50	33.1	887	1	IF2_CHLCV	Q823f2 chlamydophi
14	49	32.5	890	1	IF2_CHLPN	Q9z8m1 chlamydia p
15	49	32.5	892	1	IF2_CHLTR	O84098 chlamydia t
16	49	32.5	896	1	IF2_CHLMU	Q9pku0 chlamydia m
17	48	31.8	539	1	TCPD_HUMAN	P50991 homo sapien
18	48	31.8	539	1	TCPD_MOUSE	P80315 mus musculu
19	48	31.8	601	1	SG2_RANRI	P30945 rana ridibu
20	48	31.8	605	1	DYI4_HUMAN	Q9gzs0 homo sapien
21	47	31.1	528	1	TCPD_YEAST	P39078 saccharomyc
22	47	31.1	533	1	TCPD_AEDTR	Q9nb32 aedes trise
23	47	31.1	880	1	IF2_LEPIN	Q8f7k1 leptospira
24	46.5	30.8	350	1	CMTG_PSEPU	Q51983 pseudomonas
25	46	30.5	536	1	TCPD_FUGRU	P53451 fugu rubrip
26	46	30.5	874	1	SYA_PASMU	P57933 pasteurella
27	45	29.8	281	1	VPM_BPHP1	P51721 bacteriopha
28	45	29.8	358	1	RNFD_RHOCA	Q52715 rhodobacter
29	45	29.8	360	1	GCST_PSEPK	Q88ci7 pseudomonas
30	45	29.8	401	1	CATF_ACICA	Q43935 acinetobact
31	45	29.8	401	1	PCAF_ACICA	Q43974 acinetobact
32	45	29.8	415	1	PGK_SULTO	Q971k1 sulfolobus
33	45	29.8	429	1	PUR2_VIBCH	Q9kv81 vibrio chol
34	45	29.8	431	1	PUR2_XANCP	Q8pd48 xanthomonas
35	45	29.8	440	1	ZM10_HUMAN	O75800 homo sapien
36	45	29.8	529	1	YB53_METTH	O27221 methanobact
37	45	29.8	829	1	IF2_HAEIN	P44323 haemophilus
38	45	29.8	1248	1	NLFA_DROME	Q86np2 drosophila
39	44.5	29.5	521	1	TRPE_BUCAI	Q44695 buchnera ap
40	44.5	29.5	838	1	PTF1_XANCP	P45597 x multiphos
41	44	29.1	272	1	RFXA_HUMAN	O00287 homo sapien
42	44	29.1	329	1	Y146_HAEIN	P44542 haemophilus
43	44	29.1	407	1	K1M2_MOUSE	Q62168 mus musculu
44	44	29.1	543	1	THSB_THEAC	P48425 thermoplasm
45	44	29.1	628	1	GIDA_WIGBR	Q8d3k0 wiggleswort

ALIGNMENTS

RESULT 1
IKKB_HUMAN
ID IKKB_HUMAN STANDARD; PRT; 756 AA.
AC O14920; O75327;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
DE (I-kappa-B-kinase beta) (IkBKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
DE 2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIKB).
GN IKBKB OR IKKB.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44; SER-177 AND SER-181.
RC TISSUE=Cervical carcinoma;
RX MEDLINE=98008813; PubMed=9346484;
RA Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
RA Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
RT "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
RT NF-kappaB activation.";
RL Science 278:860-866(1997).
RN [2]
RP SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RX MEDLINE=98008814; PubMed=9346485;
RA Woronicz J.D., Gao X., Cao Z., Rothe M., Goeddel D.V.;
RT "IkappaB kinase-beta: NF-kappaB activation and complex formation with
RT IkappaB kinase-alpha and NIK.";
RL Science 278:866-869(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=99032998; PubMed=9813230;
RA Hu M.C.-T., Wang Y.-P.;
RT "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
RT embryonic tissues but localized to different human chromosomes.";
RL Gene 222:31-40(1998).
RN [4]
RP SEQUENCE FROM N.A., AND GENE MAPPING.
RX MEDLINE=98438415; PubMed=9763654;
RA Shindo M., Nakano H., Sakon S., Yagita H., Mihara M., Okumura K.;
RT "Assignment of IkappaB kinase beta (IKBKB) to human chromosome band
RT 8p12-->p11 by in situ hybridization.";
RL Cytogenet. Cell Genet. 82:32-33(1998).
RN [5]
RP SEQUENCE OF 1-256 FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

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RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length
RT   human and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   IKK PHOSPHORYLATION.
RX   MEDLINE=99038238; PubMed=9819420;
RA   Nemoto S., DiDonato J.A., Lin A.;
RT   "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT   kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL   Mol. Cell. Biol. 18:7336-7343(1998).
RN   [7]
RP   REVIEW.
RX   MEDLINE=20178139; PubMed=10712233;
RA   Jobin C., Sartor R.B.;
RT   "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT   inflammation and protection.";
RL   Am. J. Physiol. 278:C451-C462(2000).
RN   [8]
RP   IDENTIFICATION IN A COMPLEX WITH CREBBP; NCOA2; NCOA3; IKKA AND IKBKG.
RX   MEDLINE=21968797; PubMed=11971985;
RA   Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
RA   O'Malley B.W.;
RT   "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
RT   activity by I kappa B kinase.";
RL   Mol. Cell. Biol. 22:3549-3561(2002).
CC   -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC       the dissociation of the inhibitor/NF-kappa-B complex and
CC       ultimately the degradation of the inhibitor. Also phosphorylates
CC       NCOA3 (By similarity).
CC   -!- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
CC       also as a homodimer. Directly interacts with IKK-gamma/NEMO.
CC       Heterodimers form the active complex. The tripartite complex can
CC       also bind to MEKK1, MAP3K14/NIK, IKAP and IKB-alpha-p65-p50
CC       complex. Phosphorylated IKB-alpha is further released from the
CC       complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKBKG
CC       and CREBBP.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- TISSUE SPECIFICITY: Highly expressed in heart, placenta, skeletal
CC       muscle, kidney, pancreas, spleen, thymus, prostate, testis and
CC       peripheral blood.
CC   -!- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
CC       Weakly autophosphorylated.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       IKAPPAB KINASE SUBFAMILY.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   ---------------------------------------------------------------------
DR   EMBL; AF029684; AAC51860.1; -.
DR   EMBL; AF080158; AAD08997.1; -.
DR   EMBL; AF031416; AAC64675.1; -.
DR   EMBL; BC006231; AAH06231.1; -.
DR   HSSP; Q63450; 1A06.
DR   Genew; HGNC:5960; IKBKB.
DR   MIM; 603258; -.
DR   GO; GO:0005737; C:cytoplasm; NAS.
DR   GO; GO:0005524; F:ATP binding; NAS.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; NAS.
DR   GO; GO:0016563; F:transcriptional activator activity; NAS.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; NAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   Pfam; PF00069; pkinase; 1.
DR   Pfam; PF00240; ubiquitin; 1.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Phosphorylation.
FT   DOMAIN       15    300       PROTEIN KINASE.
FT   DOMAIN      458    479       LEUCINE-ZIPPER (POTENTIAL).
FT   DOMAIN      737    742       NEMO-BINDING.
FT   NP_BIND      21     29       ATP (BY SIMILARITY).
FT   BINDING      44     44       ATP (BY SIMILARITY).
FT   ACT_SITE    145    145       BY SIMILARITY.
FT   MOD_RES      23     23       PHOSPHORYLATION (BY SIMILARITY).
FT   MOD_RES     177    177       PHOSPHORYLATION.
FT   MOD_RES     181    181       PHOSPHORYLATION.
FT   MUTAGEN      44     44       K->A: LOSS OF KINASE ACTIVITY AND NO
FT                                 EFFECT ON BINDING TO NIK.
FT   MUTAGEN     177    177       S->A: DECREASE OF ACTIVITY.
FT   MUTAGEN     177    177       S->E: FULL ACTIVATION.
FT   MUTAGEN     181    181       S->A: DECREASE OF ACTIVITY.
FT   MUTAGEN     181    181       S->E: FULL ACTIVATION.
FT   CONFLICT    231    255       WHSKVRQKSEVDIVVSEDLNGTVKF -> CVRMWPGTVAHS
FT                                 CNPSTLGGRGRWI (IN REF. 5).
FT   CONFLICT    425    425       Q -> H (IN REF. 1).
SQ   SEQUENCE   756 AA;  86563 MW;  F9CADF671AE9E14E CRC64;

  Query Match             100.0%;  Score 151;  DB 1;  Length 756;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-15;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ||||||||||||||||||||||||||||||
Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


RESULT 2
IKKB_MOUSE
ID   IKKB_MOUSE     STANDARD;      PRT;   757 AA.
AC   O88351; Q9R1J6;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
DE   (I-kappa-B-kinase beta) (IkBKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
DE   2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIKB).
GN   IKBKB OR IKKB.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A., AND PHOSPHORYLATION BY MEKK1.
RC   STRAIN=C57BL/6; TISSUE=Spleen;
RX   MEDLINE=98188238; PubMed=9520401;
RA   Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
RA   Okumura K.;
RT   "Differential regulation of IkappaB kinase alpha and beta by two
RT   upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
RT   protein kinase/ERK kinase kinase-1.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Hu M.C.-T., Wang Y.-P., Mikhail A., Qiu W.R.;
RT   "Murine IkB kinase-B, a developmentally regulated protein kinase that
RT   constitutively phosphorylates serine residues of IkB.";
RL   Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
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RN   [3]
RP   DEVELOPMENTAL STAGE.
RX   MEDLINE=99455228; PubMed=10523828;
RA   Hu M.C.-T., Wang Y.-P., Qiu W.R., Mikhail A., Meyer C.F., Tan T.-H.;
RT   "Hematopoietic progenitor kinase-1 (HPK1) stress response signaling
RT   pathway activates IkappaB kinases (IKK-alpha/beta) and IKK-beta is a
RT   developmentally regulated protein kinase.";
RL   Oncogene 18:5514-5524(1999).
RN   [4]
RP   IKK PHOSPHORYLATION.
RX   MEDLINE=99038238; PubMed=9819420;
RA   Nemoto S., DiDonato J.A., Lin A.;
RT   "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT   kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL   Mol. Cell. Biol. 18:7336-7343(1998).
RN   [5]
RP   REVIEW.
RX   MEDLINE=20178139; PubMed=10712233;
RA   Jobin C., Sartor R.B.;
RT   "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT   inflammation and protection.";
RL   Am. J. Physiol. 278:C451-C462(2000).
CC   -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC       the dissociation of the inhibitor/NF-kappa-B complex and
CC       ultimately the degradation of the inhibitor. Also phosphorylates
CC       NCOA3.
CC   -!- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
CC       also as a homodimer. Directly interacts with IKK-gamma/NEMO.
CC       Heterodimers form the active complex. The tripartite complex can
CC       also bind to MEKK1, MAP3K14/NIK, IKAP and IKB-alpha-p65-p50
CC       complex. Phosphorylated IKB-alpha is further released from the
CC       complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKBKG
CC       and CREBBP (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- TISSUE SPECIFICITY: Expressed in liver, kidney and spleen.
CC   -!- DEVELOPMENTAL STAGE: While it is expressed ubiquitously throughout
CC       the mouse embryo, at E9.5 day its expression begins to be
CC       localized to the brain, neural ganglia, neural tube, and in liver
CC       at E12.5 day. At E15.5 day, the expression is further restricted
CC       to specific tissues of the embryo.
CC   -!- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
CC       Weakly autophosphorylated.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       IKAPPAB KINASE SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF026524; AAC23557.1; -.
DR   EMBL; AF088910; AAD52095.1; -.
DR   HSSP; Q63450; 1A06.
DR   MGD; MGI:1338071; Ikbkb.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Phosphorylation.
FT   DOMAIN       15    300       PROTEIN KINASE.
FT   DOMAIN      458    479       LEUCINE-ZIPPER (POTENTIAL).
FT   DOMAIN      737    742       NEMO-BINDING.
FT   NP_BIND      21     29       ATP (BY SIMILARITY).
FT   BINDING      44     44       ATP (BY SIMILARITY).
FT   ACT_SITE    145    145       BY SIMILARITY.
FT   MOD_RES      23     23       PHOSPHORYLATION (BY SIMILARITY).
FT   MOD_RES     177    177       PHOSPHORYLATION (BY SIMILARITY).
FT   MOD_RES     181    181       PHOSPHORYLATION (BY SIMILARITY).
FT   CONFLICT     56     56       N -> D (IN REF. 2).
FT   CONFLICT    343    343       N -> D (IN REF. 2).
FT   CONFLICT    356    356       K -> E (IN REF. 2).
FT   CONFLICT    390    390       L -> F (IN REF. 2).
FT   CONFLICT    406    406       P -> Q (IN REF. 2).
FT   CONFLICT    573    573       K -> R (IN REF. 2).
FT   CONFLICT    736    757       TLDWSWLQMEDEERCSLEQACD -> VTA (IN REF.
FT                                2).
SQ   SEQUENCE   757 AA;  86690 MW;  FED962F095449C5E CRC64;

  Query Match             100.0%;  Score 151;  DB 1;  Length 757;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-15;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ||||||||||||||||||||||||||||||
Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


RESULT 3
IKBB_RAT
ID   IKBB_RAT       STANDARD;      PRT;   757 AA.
AC   Q9QY78;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Inhibitor of nuclear factor kappa B kinase beta subunit (EC 2.7.1.-)
DE   (I-kappa-B-kinase beta) (IkBKB) (IKK-beta) (IKK-B) (I-kappa-B kinase
DE   2) (IKK2) (Nuclear factor NF-kappa-B inhibitor kinase beta) (NFKBIKB).
GN   IKBKB OR IKKB.
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Zhang Y., Sun S., Ravid K.;
RT   "IKK beta in megakaryocyte differentiation.";
RL   Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   IKK PHOSPHORYLATION.
RX   MEDLINE=99038238; PubMed=9819420;
RA   Nemoto S., DiDonato J.A., Lin A.;
RT   "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT   kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL   Mol. Cell. Biol. 18:7336-7343(1998).
RN   [3]
RP   REVIEW.
RX   MEDLINE=20178139; PubMed=10712233;
RA   Jobin C., Sartor R.B.;
RT   "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT   inflammation and protection.";
RL   Am. J. Physiol. 278:C451-C462(2000).
CC   -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC       the dissociation of the inhibitor/NF-kappa-B complex and
CC       ultimately the degradation of the inhibitor. Also phosphorylates
CC       NCOA3.
CC   -!- SUBUNIT: Preferentially found as a heterodimer with IKK-alpha but
CC       also as a homodimer. Directly interacts with IKK-gamma/NEMO.
CC       Heterodimers form the active complex. The tripartite complex can
CC       also bind to MEKK1, MAP3K14/NIK, IKAP and IKB-alpha-p65-p50
CC       complex. Phosphorylated IKB-alpha is further released from the
CC       complex. Found in a complex composed of NCOA2, NCOA3, IKKA, IKBKG
CC       and CREBBP (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- PTM: Phosphorylated by MEKK1 and probably also by MAP3K14/NIK.
CC       Weakly autophosphorylated.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       IKAPPAB KINASE SUBFAMILY.
```

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CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF115282; AAF21978.1; -.
DR   HSSP; Q63450; 1A06.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; FALSE_NEG.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Phosphorylation.
FT   DOMAIN       15    300       PROTEIN KINASE.
FT   DOMAIN      458    479       LEUCINE-ZIPPER (POTENTIAL).
FT   DOMAIN      737    742       NEMO-BINDING.
FT   NP_BIND      21     29       ATP (BY SIMILARITY).
FT   BINDING      44     44       ATP (BY SIMILARITY).
FT   ACT_SITE    145    145       BY SIMILARITY.
FT   MOD_RES      23     23       PHOSPHORYLATION (BY SIMILARITY).
FT   MOD_RES     177    177       PHOSPHORYLATION (BY SIMILARITY).
FT   MOD_RES     181    181       PHOSPHORYLATION (BY SIMILARITY).
SQ   SEQUENCE   757 AA;  86866 MW;  3AFFE46A7DF91F9C CRC64;

  Query Match            100.0%;  Score 151;  DB 1;  Length 757;
  Best Local Similarity   100.0%;  Pred. No. 4.1e-15;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              |||||||||||||||||||||||||||||
Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


RESULT 4
IKKA_MOUSE
ID   IKKA_MOUSE     STANDARD;      PRT;   745 AA.
AC   Q60680; Q9D2X3;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)
DE   (I kappa-B kinase alpha) (IkBKA) (IKK-alpha) (IKK-A) (IkappaB kinase)
DE   (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
DE   kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKBIKA).
GN   CHUK OR IKKA.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   STRAIN=BALB/c;
RX   MEDLINE=96044444; PubMed=7558004;
RA   Mock B.A., Connelly M.A., McBride O.W., Kozak C.A., Marcu K.B.;
RT   "CHUK, a conserved helix-loop-helix ubiquitous kinase, maps to human
RT   chromosome 10 and mouse chromosome 19.";
RL   Genomics 27:348-351(1995).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   STRAIN=BALB/c;
RX   MEDLINE=96258427; PubMed=8777433;
RA   Connelly M.A., Marcu K.B.;
RT   "CHUK, a new member of the helix-loop-helix and leucine zipper
RT   families of interacting proteins, contains a serine-threonine kinase
RT   catalytic domain.";
RL   Cell. Mol. Biol. Res. 41:537-549(1996).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 3).
RC   STRAIN=C57BL/6J; TISSUE=Colon;
RX   MEDLINE=21085660; PubMed=11217851;
RA   Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA   Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA   Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA   Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA   Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA   Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA   Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA   Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA   Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA   Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA   Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA   Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA   Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA   Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA   Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA   Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA   Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA   Hayashizaki Y.;
RT   "Functional annotation of a full-length mouse cDNA collection.";
RL   Nature 409:685-690(2001).
RN   [4]
RP   ALTERNATIVE SPLICING.
RX   MEDLINE=20198447; PubMed=10733566;
RA   McKenzie F.R., Connelly M.A., Balzarano D., Mueller J.R.,
RA   Geleziunas R., Marcu K.B.;
RT   "Functional isoforms of IkappaB kinase alpha (IKKalpha) lacking
RT   leucine zipper and helix-loop-helix domains reveal that IKKalpha and
RT   IKKbeta have different activation requirements.";
RL   Mol. Cell. Biol. 20:2635-2649(2000).
RN   [5]
RP   PHOSPHORYLATION BY MAP3K14/NIK.
RX   MEDLINE=98188238; PubMed=9520401;
RA   Nakano H., Shindo M., Sakon S., Nishinaka S., Mihara M., Yagita H.,
RA   Okumura K.;
RT   "Differential regulation of IkappaB kinase alpha and beta by two
RT   upstream kinases, NF-kappaB-inducing kinase and mitogen-activated
RT   protein kinase/ERK kinase kinase-1.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:3537-3542(1998).
RN   [6]
RP   IKKA-IKKB BINDING.
RX   MEDLINE=99212141; PubMed=10195894;
RA   Delhase M., Hayakawa M., Chen Y., Karin M.;
RT   "Positive and negative regulation of IkappaB kinase activity through
RT   IKKbeta subunit phosphorylation.";
RL   Science 284:309-313(1999).
RN   [7]
RP   IKK PHOSPHORYLATION.
RX   MEDLINE=99038238; PubMed=9819420;
RA   Nemoto S., DiDonato J.A., Lin A.;
RT   "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT   kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL   Mol. Cell. Biol. 18:7336-7343(1998).
RN   [8]
RP   REVIEW.
RX   MEDLINE=20178139; PubMed=10712233;
RA   Jobin C., Sartor R.B.;
RT   "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT   inflammation and protection.";
RL   Am. J. Physiol. 278:C451-C462(2000).
CC   -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC       the dissociation of the inhibitor/NF-kappa-B complex and
CC       ultimately the degradation of the inhibitor. Also phosphorylates
CC       NCOA3.
CC   -!- ENZYME REGULATION: Activated when phosphorylated and inactivated
CC       when dephosphorylated.
CC   -!- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
CC       also as an homodimer. Directly interacts with IKK-gamma/NEMO.
```

```
CC       Heterodimers form the active complex. The tripartite complex can
CC       also bind to MAP3K14/NIK, MEKK1, IKAP and IKB-alpha-p65-p50
CC       complex. A weak interaction with TRAF2 cannot be excluded. Part of
CC       a complex composed of NCOA2, NCOA3, IKKB, IKBKG and CREBBP (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=1;
CC         IsoId=Q60680-1; Sequence=Displayed;
CC       Name=2; Synonyms=Delta LH;
CC         IsoId=Q60680-2; Sequence=VSP_004866, VSP_004867;
CC       Name=3; Synonyms=Delta H;
CC         IsoId=Q60680-3; Sequence=VSP_004868, VSP_004869;
CC   -!- TISSUE SPECIFICITY: Ubiquitous only for isoform 1, isoforms 2 and
CC       3 are expressed predominantly in brain and T-lymphocytes.
CC   -!- DEVELOPMENTAL STAGE: Maximally expressed at E7 day followed by
CC       E11, E15 and E17 days. In the limb development, its expression
CC       predominates in the limb buds at E12.5 day.
CC   -!- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
CC       MEKK1, and dephosphorylated by PP2A. Autophosphorylated.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       IKAPPAB KINASE SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U12473; AAC52589.1; -.
DR   EMBL; AK018671; BAB31335.1; -.
DR   PIR; I49101; I49101.
DR   HSSP; Q63450; 1A06.
DR   MGD; MGI:99484; Chuk.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Phosphorylation; Alternative splicing.
FT   DOMAIN       15    300       PROTEIN KINASE.
FT   DOMAIN      455    476       LEUCINE-ZIPPER (POTENTIAL).
FT   DOMAIN      738    743       NEMO-BINDING.
FT   NP_BIND      21     29       ATP (BY SIMILARITY).
FT   BINDING      44     44       ATP (BY SIMILARITY).
FT   ACT_SITE    144    144       BY SIMILARITY.
FT   MOD_RES      23     23       PHOSPHORYLATION (BY PKB/AKT1)
FT                                (BY SIMILARITY).
FT   MOD_RES     176    176       PHOSPHORYLATION (BY MAP3K14)
FT                                (BY SIMILARITY).
FT   VARSPLIC    452    471       MLSLLRYNANLTKMKNTLIS -> IFRKNVKSMERNGRKGH
FT                                SLF (in isoform 2).
FT                                /FTId=VSP_004866.
FT   VARSPLIC    472    745       Missing (in isoform 2).
FT                                /FTId=VSP_004867.
FT   VARSPLIC    577    584       DHLYSDST -> GKTLQSQY (in isoform 3).
FT                                /FTId=VSP_004868.
FT   VARSPLIC    585    745       Missing (in isoform 3).
FT                                /FTId=VSP_004869.
FT   CONFLICT    236    236       K -> E (IN REF. 3).
FT   CONFLICT    400    400       S -> Y (IN REF. 3).
SQ   SEQUENCE   745 AA;  84728 MW;  3FEF5582AFF92233 CRC64;

  Query Match             55.6%;  Score 84;  DB 1;  Length 745;
  Best Local Similarity   46.7%;  Pred. No. 6.9e-05;

    Matches   14;  Conservative   11;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              :::|:| |:|::||:|| ||:||  :: ||
Db        532 DQIMSLHTEIMELQKSPYGRRQGDLMESLE 561


RESULT 5
IKKA_HUMAN
ID   IKKA_HUMAN     STANDARD;      PRT;   745 AA.
AC   O15111; O14666; Q13132; Q92467;
DT   16-OCT-2001 (Rel. 40, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Inhibitor of nuclear factor kappa-B kinase alpha subunit (EC 2.7.1.-)
DE   (I kappa-B kinase alpha) (IkBKA) (IKK-alpha) (IKK-A) (IkappaB kinase)
DE   (I-kappa-B kinase 1) (IKK1) (Conserved helix-loop-helix ubiquitous
DE   kinase) (Nuclear factor NFkappaB inhibitor kinase alpha) (NFKBIKA).
GN   CHUK OR IKKA.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., AND MUTAGENESIS OF LYS-44.
RC   TISSUE=T-cell;
RX   MEDLINE=97386461; PubMed=9244310;
RA   Regnier C.H., Song H.Y., Gao X., Goeddel D.V., Cao Z., Rothe M.;
RT   "Identification and characterization of an IkappaB kinase.";
RL   Cell 90:373-383(1997).
RN   [2]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX   MEDLINE=97394468; PubMed=9252186;
RA   DiDonato J.A., Hayakawa M., Rothwarf D.M., Zandi E., Karin M.;
RT   "A cytokine-responsive IkappaB kinase that activates the transcription
RT   factor NF-kappaB.";
RL   Nature 388:548-554(1997).
RN   [3]
RP   SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND MUTAGENESIS OF LYS-44 AND
RP   SER-176.
RC   TISSUE=Cervical carcinoma;
RX   MEDLINE=98008813; PubMed=9346484;
RA   Mercurio F., Zhu H., Murray B.W., Shevchenko A., Bennett B.L.,
RA   Li J.W., Young D.B., Barbosa M., Mann M., Manning A., Rao A.;
RT   "IKK-1 and IKK-2: cytokine-activated IkappaB kinases essential for
RT   NF-kappaB activation.";
RL   Science 278:860-866(1997).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Heart;
RX   MEDLINE=99032998; PubMed=9813230;
RA   Hu M.C.-T., Wang Y.-P.;
RT   "IkappaB kinase-alpha and -beta genes are coexpressed in adult and
RT   embryonic tissues but localized to different human chromosomes.";
RL   Gene 222:31-40(1998).
RN   [5]
RP   SEQUENCE OF 32-745 FROM N.A.
RC   TISSUE=Cervical carcinoma;
RX   MEDLINE=96258427; PubMed=8777433;
RA   Connelly M.A., Marcu K.B.;
RT   "CHUK, a new member of the helix-loop-helix and leucine zipper
RT   families of interacting proteins, contains a serine-threonine kinase
RT   catalytic domain.";
RL   Cell. Mol. Biol. Res. 41:537-549(1995).
RN   [6]
RP   PHOSPHORYLATION BY MAP3K14/NIK, AND MUTAGENESIS OF SER-176; THR-179
RP   AND SER-180.
RX   MEDLINE=98188283; PubMed=9520446;
RA   Ling L., Cao Z., Goeddel D.V.;
RT   "NF-kappaB-inducing kinase activates IKK-alpha by phosphorylation of
RT   Ser-176.";
RL   Proc. Natl. Acad. Sci. U.S.A. 95:3792-3797(1998).
RN   [7]
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RP   PHOSPHORYLATION BY AKT, AND MUTAGENESIS OF THR-23.
RX   MEDLINE=99413720; PubMed=10485710;
RA   Ozes O.N., Mayo L.D., Gustin J.A., Pfeffer S.R., Pfeffer L.M.,
RA   Donner D.B.;
RT   "NF-kappaB activation by tumour necrosis factor requires the Akt
RT   serine-threonine kinase.";
RL   Nature 401:82-85(1999).
RN   [8]
RP   IKKA-IKKB BINDING.
RX   MEDLINE=99212141; PubMed=10195894;
RA   Delhase M., Hayakawa M., Chen Y., Karin M.;
RT   "Positive and negative regulation of IkappaB kinase activity through
RT   IKKbeta subunit phosphorylation.";
RL   Science 284:309-313(1999).
RN   [9]
RP   IKK PHOSPHORYLATION.
RX   MEDLINE=99038238; PubMed=9819420;
RA   Nemoto S., DiDonato J.A., Lin A.;
RT   "Coordinate regulation of IkappaB kinases by mitogen-activated protein
RT   kinase kinase kinase 1 and NF-kappaB-inducing kinase.";
RL   Mol. Cell. Biol. 18:7336-7343(1998).
RN   [10]
RP   REVIEW.
RX   MEDLINE=20178139; PubMed=10712233;
RA   Jobin C., Sartor R.B.;
RT   "The I kappa B/NF-kappa B system: a key determinant of mucosal
RT   inflammation and protection.";
RL   Am. J. Physiol. 278:C451-C462(2000).
RN   [11]
RP   SUBUNIT OF A COMPLEX CONTAINING CREBBP; NCOA2; NCOA3; IKKB AND IKBKG.
RX   MEDLINE=21968797; PubMed=11971985;
RA   Wu R.C., Qin J., Hashimoto Y., Wong J., Xu J., Tsai S.Y., Tsai M.J.,
RA   O'Malley B.W.;
RT   "Regulation of SRC-3 (pCIP/ACTR/AIB-1/RAC-3/TRAM-1) coactivator
RT   activity by I kappa B kinase.";
RL   Mol. Cell. Biol. 22:3549-3561(2002).
CC   -!- FUNCTION: Phosphorylates inhibitors of NF-kappa-B thus leading to
CC       the dissociation of the inhibitor/NF-kappa-B complex and
CC       ultimately the degradation of the inhibitor. Also phosphorylates
CC       NCOA3.
CC   -!- ENZYME REGULATION: Activated when phosphorylated and inactivated
CC       when dephosphorylated.
CC   -!- SUBUNIT: Preferentially found as a heterodimer with IKK-beta but
CC       also as an homodimer. Directly interacts with IKK-gamma/NEMO.
CC       Heterodimers form the active complex. The tripartite complex can
CC       also bind to MAP3K14/NIK, MEKK1, IKAP and IKB-alpha-p65-p50
CC       complex. A weak interaction with TRAF2 cannot be excluded. Part of
CC       a complex composed of NCOA2, NCOA3, IKKB, IKBKG and CREBBP.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- TISSUE SPECIFICITY: Widely expressed.
CC   -!- PTM: Phosphorylated by MAP3K14/NIK, AKT and to a lesser extent by
CC       MEKK1, and dephosphorylated by PP2A. Autophosphorylated.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC       IKAPPAB KINASE SUBFAMILY.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF012890; AAC51662.1; -.
DR   EMBL; AF009225; AAC51671.1; -.
DR   EMBL; AF080157; AAD08996.1; -.
DR   EMBL; U22512; AAC50713.1; -.
DR   HSSP; Q63450; 1A06.
DR   Genew; HGNC:1974; CHUK.
DR   MIM; 600664; -.
DR   GO; GO:0005737; C:cytoplasm; TAS.
DR   GO; GO:0008384; F:IkappaB kinase activity; TAS.
DR   GO; GO:0007345; P:embryogenesis and morphogenesis; TAS.
DR   GO; GO:0007252; P:I-kappaB phosphorylation; TAS.
DR   GO; GO:0006955; P:immune response; TAS.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
KW   Transferase; Serine/threonine-protein kinase; ATP-binding;
KW   Phosphorylation.
FT   DOMAIN       15    302       PROTEIN KINASE.
FT   DOMAIN      455    476       LEUCINE-ZIPPER (POTENTIAL).
FT   DOMAIN      738    743       NEMO-BINDING.
FT   NP_BIND      21     29       ATP (BY SIMILARITY).
FT   BINDING      44     44       ATP (BY SIMILARITY).
FT   ACT_SITE    144    144       BY SIMILARITY.
FT   MOD_RES      23     23       PHOSPHORYLATION (BY PKB/AKT1).
FT   MOD_RES     176    176       PHOSPHORYLATION (BY MAP3K14).
FT   MUTAGEN      23     23       T->A: LOSS OF PHOSPHORYLATION AND
FT                                DECREASE OF KINASE ACTIVITY.
FT   MUTAGEN      44     44       K->A: LOSS OF KINASE ACTIVITY.
FT   MUTAGEN      44     44       K->M: LOSS OF AUTOPHOSPHORYLATION.
FT   MUTAGEN     176    176       S->A: LOSS OF PHOSPHORYLATION AND OF
FT                                ACTIVITY.
FT   MUTAGEN     176    176       S->E: FULL ACTIVATION.
FT   MUTAGEN     179    179       T->A: NO CHANGE IN PHOSPHORYLATION.
FT   MUTAGEN     180    180       S->A: NO CHANGE IN PHOSPHORYLATION.
FT   CONFLICT    543    543       E -> G (IN REF. 2).
FT   CONFLICT    604    604       L -> R (IN REF. 5).
FT   CONFLICT    679    680       TS -> AY (IN REF. 5).
FT   CONFLICT    684    684       P -> A (IN REF. 3 AND 5).
FT   CONFLICT    686    687       TS -> DL (IN REF. 5).
SQ   SEQUENCE   745 AA;  84653 MW;  7A90B59BC98A56C2 CRC64;

  Query Match             52.3%;  Score 79;  DB 1;  Length 745;
  Best Local Similarity   43.3%;  Pred. No. 0.0004;
  Matches   13;  Conservative   11;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              :::|:|  :|::||:|| ||:||  :: ||
Db        532 DQIMSLHAEIMELQKSPYGRRQGDLMESLE 561


RESULT 6
THIK_ECO57
ID   THIK_ECO57     STANDARD;      PRT;   387 AA.
AC   Q8X8J4;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Fatty oxidation complex beta
DE   subunit) (Beta-ketothiolase) (Acetyl-CoA acyltransferase).
GN   FADA OR Z5366 OR ECS4773.
OS   Escherichia coli O157:H7.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=83334;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / EDL933 / ATCC 700927;
RX   MEDLINE=21074935; PubMed=11206551;
RA   Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,
RA   Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
RA   Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,
RA   Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,
RA   Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,
RA   Welch R.A., Blattner F.R.;
RT   "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";
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RL   Nature 409:529-533(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O157:H7 / RIMD 0509952;
RX   MEDLINE=21156231; PubMed=11258796;
RA   Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,
RA   Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,
RA   Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T.,
RA   Kuhara S., Shiba T., Hattori M., Shinagawa H.;
RT   "Complete genome sequence of enterohemorrhagic Escherichia coli
RT   O157:H7 and genomic comparison with a laboratory strain K-12.";
RL   DNA Res. 8:11-22(2001).
CC   -!- FUNCTION: FadB and fadA are the alpha and beta subunits of the
CC       multifunctional enzyme complex of the fatty acid degradation
CC       cycle (By similarity).
CC   -!- CATALYTIC ACTIVITY: Acyl-CoA + acetyl-CoA = CoA + 3-oxoacyl-CoA.
CC   -!- PATHWAY: Fatty acid beta-oxidation cycle; third step.
CC   -!- SUBUNIT: Tetramer of two alpha chains and two beta chains (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: Belongs to the thiolase family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AE005615; AAG59039.1; -.
DR   EMBL; AP002567; BAB38196.1; -.
DR   PIR; C86072; C86072.
DR   PIR; E91225; E91225.
DR   InterPro; IPR002155; Thiolase.
DR   Pfam; PF00108; thiolase; 1.
DR   Pfam; PF02803; thiolase_C; 1.
DR   PROSITE; PS00098; THIOLASE_1; 1.
DR   PROSITE; PS00737; THIOLASE_2; 1.
DR   PROSITE; PS00099; THIOLASE_3; 1.
KW   Fatty acid metabolism; Transferase; Acyltransferase;
KW   Complete proteome.
FT   ACT_SITE     91     91       SUBSTRATE BINDING (BY SIMILARITY).
FT   ACT_SITE    373    373       BASE (BY SIMILARITY).
SQ   SEQUENCE   387 AA;  40841 MW;  98D3879B30B46CCC CRC64;

  Query Match             35.8%;  Score 54;  DB 1;  Length 387;
  Best Local Similarity   61.1%;  Pred. No. 1.3;
  Matches   11;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          7 QTDIVDLQRSPMGRKQGG 24
              |  |||  |:|||| :||
Db          3 QVVIVDAIRTPMGRSKGG 20


RESULT 7
THIK_ECOLI
ID   THIK_ECOLI     STANDARD;      PRT;   387 AA.
AC   P21151; P78130;
DT   01-MAY-1991 (Rel. 18, Created)
DT   01-AUG-1992 (Rel. 23, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Fatty oxidation complex beta
DE   subunit) (Beta-ketothiolase) (Acetyl-CoA acyltransferase).
GN   FADA OR OLDA OR B3845.
OS   Escherichia coli.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=562;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=92358234; PubMed=1379743;
RA   Daniels D.L., Plunkett G. III, Burland V.D., Blattner F.R.;
RT   "Analysis of the Escherichia coli genome: DNA sequence of the region
RT   from 84.5 to 86.5 minutes.";
RL   Science 257:771-778(1992).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91035260; PubMed=1699931;
RA   Dirusso C.C.;
RT   "Primary sequence of the Escherichia coli fadBA operon, encoding the
RT   fatty acid-oxidizing multienzyme complex, indicates a high degree of
RT   homology to eucaryotic enzymes.";
RL   J. Bacteriol. 172:6459-6468(1990).
RN   [3]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 1-10.
RC   STRAIN=K12;
RX   MEDLINE=90285166; PubMed=2191949;
RA   Yang S.-Y., Yang X.-Y.H., Healy-Louie G., Schulz H., Elzinga M.;
RT   "Nucleotide sequence of the fadA gene. Primary structure of
RT   3-ketoacyl-coenzyme A thiolase from Escherichia coli and the
RT   structural organization of the fadAB operon.";
RL   J. Biol. Chem. 265:10424-10429(1990).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / W3110;
RX   MEDLINE=90370500; PubMed=2204034;
RA   Nakahigashi K., Inokuchi H.;
RT   "Nucleotide sequence of the fadA and fadB genes from Escherichia
RT   coli.";
RL   Nucleic Acids Res. 18:4937-4937(1990).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   STRAIN=K12 / MG1655;
RX   MEDLINE=97426617; PubMed=9278503;
RA   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA   Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA   Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA   Mau B., Shao Y.;
RT   "The complete genome sequence of Escherichia coli K-12.";
RL   Science 277:1453-1474(1997).
CC   -!- FUNCTION: FadB and fadA are the alpha and beta subunits of the
CC       multifunctional enzyme complex of the fatty acid degradation
CC       cycle.
CC   -!- CATALYTIC ACTIVITY: Acyl-CoA + acetyl-CoA = CoA + 3-oxoacyl-CoA.
CC   -!- PATHWAY: Fatty acid beta-oxidation cycle; third step.
CC   -!- SUBUNIT: Tetramer of two alpha chains and two beta chains.
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: Belongs to the thiolase family.
CC   ----------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; M87049; AAA67642.1; -.
DR   EMBL; M59368; AAA23751.1; -.
DR   EMBL; X52837; CAB40810.1; -.
DR   EMBL; M74164; AAA62778.1; -.
DR   EMBL; AE000460; AAC76848.1; -.
DR   PIR; F65189; XUEC.
DR   HSSP; P27796; 1AFY.
DR   ECO2DBASE; H038.6; 6TH EDITION.
DR   ECO2DBASE; H038.7; 6TH EDITION.
DR   EcoGene; EG10278; fadA.
DR   InterPro; IPR002155; Thiolase.
DR   Pfam; PF00108; thiolase; 1.
DR   Pfam; PF02803; thiolase_C; 1.
DR   PROSITE; PS00098; THIOLASE_1; 1.
DR   PROSITE; PS00099; THIOLASE_3; 1.
DR   PROSITE; PS00737; THIOLASE_2; 1.
KW   Fatty acid metabolism; Transferase; Acyltransferase;
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KW   Complete proteome.
FT   ACT_SITE     91      91       SUBSTRATE BINDING (BY SIMILARITY).
FT   ACT_SITE    373     373       BASE (BY SIMILARITY).
FT   CONFLICT     37      37       T -> S (IN REF. 2 AND 3).
FT   CONFLICT    119     119       E -> G (IN REF. 4).
FT   CONFLICT    371     374       TMCI -> DGCVS (IN REF. 3).
SQ   SEQUENCE   387 AA;  40890 MW;  CB0FF8EF4597D8BA CRC64;

  Query Match             35.8%;  Score 54;  DB 1;  Length 387;
  Best Local Similarity   61.1%;  Pred. No. 1.3;
  Matches   11;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          7 QTDIVDLQRSPMGRKQGG 24
              |  |||  |:|||| :||
Db          3 QVVIVDAIRTPMGRSKGG 20


RESULT 8
THIK_SALTY
ID   THIK_SALTY     STANDARD;      PRT;   387 AA.
AC   Q9L6L6;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Fatty oxidation complex beta
DE   subunit) (Beta-ketothiolase) (Acetyl-CoA acyltransferase).
GN   FADA OR STM3982 OR STMD1.7 OR STY3578 OR T3316.
OS   Salmonella typhimurium, and
OS   Salmonella typhi.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Salmonella.
OX   NCBI_TaxID=602, 601;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   SPECIES=S.typhimurium; STRAIN=LT2 / SGSC1412 / ATCC 700720;
RX   MEDLINE=21534948; PubMed=11677609;
RA   McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,
RA   Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,
RA   Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,
RA   Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
RA   Waterston R., Wilson R.K.;
RT   "Complete genome sequence of Salmonella enterica serovar Typhimurium
RT   LT2.";
RL   Nature 413:852-856(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   SPECIES=S.typhi; STRAIN=CT18;
RX   MEDLINE=21534947; PubMed=11677608;
RA   Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.,
RA   Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
RA   Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
RA   Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
RA   Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
RA   Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
RA   Quail M.A., Rutherford K., Simmonds M., Skelton J., Stevens K.,
RA   Whitehead S., Barrell B.G.;
RT   "Complete genome sequence of a multiple drug resistant Salmonella
RT   enterica serovar Typhi CT18.";
RL   Nature 413:848-852(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   SPECIES=S.typhi; STRAIN=Ty2 / ATCC 700931;
RX   MEDLINE=22531367; PubMed=12644504;
RA   Deng W., Liou S.-R., Plunkett G. III, Mayhew G.F., Rose D.J.,
RA   Burland V., Kodoyianni V., Schwartz D.C., Blattner F.R.;
RT   "Comparative genomics of Salmonella enterica serovar Typhi strains Ty2
RT   and CT18.";
RL   J. Bacteriol. 185:2330-2337(2003).
CC   -!- FUNCTION: FadB and fadA are the alpha and beta subunits of the
CC       multifunctional enzyme complex of the fatty acid degradation
CC       cycle (By similarity).
CC   -!- CATALYTIC ACTIVITY: Acyl-CoA + acetyl-CoA = CoA + 3-oxoacyl-CoA.
CC   -!- PATHWAY: Fatty acid beta-oxidation cycle; third step.
CC   -!- SUBUNIT: Tetramer of two alpha chains and two beta chains (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: Belongs to the thiolase family.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF233324; AAF33416.1; -.
DR   EMBL; AE008886; AAL22826.1; -.
DR   EMBL; AL627278; CAD07911.1; -.
DR   EMBL; AE016845; AAO70844.1; -.
DR   HSSP; P27796; 1AFY.
DR   StyGene; SG?????; fadA.
DR   InterPro; IPR002155; Thiolase.
DR   Pfam; PF00108; thiolase; 1.
DR   Pfam; PF02803; thiolase_C; 1.
DR   PROSITE; PS00098; THIOLASE_1; 1.
DR   PROSITE; PS00737; THIOLASE_2; 1.
DR   PROSITE; PS00099; THIOLASE_3; 1.
KW   Fatty acid metabolism; Transferase; Acyltransferase;
KW   Complete proteome.
FT   ACT_SITE     91      91       SUBSTRATE BINDING (BY SIMILARITY).
FT   ACT_SITE    373     373       BASE (BY SIMILARITY).
SQ   SEQUENCE   387 AA;  41004 MW;  39E24805360ABD8A CRC64;

  Query Match             35.8%;  Score 54;  DB 1;  Length 387;
  Best Local Similarity   61.1%;  Pred. No. 1.3;
  Matches   11;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          7 QTDIVDLQRSPMGRKQGG 24
              |  |||  |:|||| :||
Db          3 QVVIVDAIRTPMGRSKGG 20


RESULT 9
THIK_PSEFR
ID   THIK_PSEFR     STANDARD;      PRT;   390 AA.
AC   P28790;
DT   01-DEC-1992 (Rel. 24, Created)
DT   01-DEC-1992 (Rel. 24, Last sequence update)
DT   01-FEB-1994 (Rel. 28, Last annotation update)
DE   3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Fatty oxidation complex beta
DE   subunit) (Beta-ketothiolase) (Acetyl-CoA acyltransferase).
GN   FAOB.
OS   Pseudomonas fragi.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=296;
RN   [1]
RP   SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC   STRAIN=B-0771;
RX   MEDLINE=92299657; PubMed=1607366;
RA   Sato S., Hayashi M., Imamura S., Ozeki Y., Kawaguchi A.;
RT   "Primary structures of the genes, faoA and faoB, from Pseudomonas
RT   fragi B-0771 which encode the two subunits of the HDT multienzyme
RT   complex involved in fatty acid beta-oxidation.";
RL   J. Biochem. 111:8-15(1992).
CC   -!- FUNCTION: FAOA AND FAOB ARE THE ALPHA AND BETA SUBUNITS OF THE
CC       MULTIFUNCTIONAL ENZYME COMPLEX OF THE FATTY ACID DEGRADATION
CC       CYCLE.
CC   -!- CATALYTIC ACTIVITY: Acyl-CoA + acetyl-CoA = CoA + 3-oxoacyl-CoA.
CC   -!- PATHWAY: Fatty acid beta-oxidation cycle.
CC   -!- SUBUNIT: Tetramer of two alpha chains and two beta chains.
CC   -!- SIMILARITY: Belongs to the thiolase family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; D10390; BAA01228.1; -.
DR   PIR; JS0624; JS0624.
DR   HSSP; P27796; 1PXT.
DR   InterPro; IPR002155; Thiolase.
DR   Pfam; PF00108; thiolase; 1.
DR   Pfam; PF02803; thiolase_C; 1.
DR   PROSITE; PS00098; THIOLASE_1; 1.
DR   PROSITE; PS00099; THIOLASE_3; 1.
DR   PROSITE; PS00737; THIOLASE_2; 1.
KW   Fatty acid metabolism; Transferase; Acyltransferase.
FT   INIT_MET      0      0
FT   ACT_SITE     94     94       SUBSTRATE BINDING (BY SIMILARITY).
FT   ACT_SITE    376    376       BASE (BY SIMILARITY).
SQ   SEQUENCE   390 AA;  41475 MW;  F9270235BCBE3D09 CRC64;

  Query Match             35.8%;  Score 54;  DB 1;  Length 390;
  Best Local Similarity   66.7%;  Pred. No. 1.3;
  Matches   10;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 IVDLQRSPMGRKQGG 24
              |||  |:|||| :||
Db          9 IVDFGRTPMGRSKGG 23


RESULT 10
THIK_YERPE
ID   THIK_YERPE     STANDARD;      PRT;   387 AA.
AC   Q8ZAM9;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   3-ketoacyl-CoA thiolase (EC 2.3.1.16) (Fatty oxidation complex beta
DE   subunit) (Beta-ketothiolase) (Acetyl-CoA acyltransferase).
GN   FADA OR YPO3767 OR Y0463.
OS   Yersinia pestis.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Yersinia.
OX   NCBI_TaxID=632;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CO-92 / Biovar Orientalis;
RX   MEDLINE=21470413; PubMed=11586360;
RA   Parkhill J., Wren B.W., Thomson N.R., Titball R.W., Holden M.T.G.,
RA   Prentice M.B., Sebaihia M., James K.D., Churcher C., Mungall K.L.,
RA   Baker S., Basham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA   Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA   Feltwell T., Hamlin N., Holroyd S., Jagels K., Karlyshev A.V.,
RA   Leather S., Moule S., Oyston P.C.F., Quail M.A., Rutherford K.,
RA   Simmonds M., Skelton J., Stevens K., Whitehead S., Barrell B.G.;
RT   "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL   Nature 413:523-527(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=KIM5 / Biovar Mediaevalis;
RX   MEDLINE=22137863; PubMed=12142430;
RA   Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA   Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA   Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA   Straley S.C., McDonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA   Perry R.D.;
RT   "Genome sequence of Yersinia pestis KIM.";
RL   J. Bacteriol. 184:4601-4611(2002).
CC   -!- FUNCTION: FadB and fadA are the alpha and beta subunits of the
CC       multifunctional enzyme complex of the fatty acid degradation
CC       cycle (By similarity).
CC   -!- CATALYTIC ACTIVITY: Acyl-CoA + acetyl-CoA = CoA + 3-oxoacyl-CoA.
CC   -!- PATHWAY: Fatty acid beta-oxidation cycle; third step.
CC   -!- SUBUNIT: Tetramer of two alpha chains and two beta chains (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC   -!- SIMILARITY: Belongs to the thiolase family.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; AJ414158; CAC93235.1; -.
DR   EMBL; AE013646; AAM84052.1; -.
DR   PIR; AG0458; AG0458.
DR   InterPro; IPR002155; Thiolase.
DR   Pfam; PF00108; thiolase; 1.
DR   Pfam; PF02803; thiolase_C; 1.
DR   PROSITE; PS00098; THIOLASE_1; 1.
DR   PROSITE; PS00737; THIOLASE_2; 1.
DR   PROSITE; PS00099; THIOLASE_3; 1.
KW   Fatty acid metabolism; Transferase; Acyltransferase;
KW   Complete proteome.
FT   ACT_SITE     91     91       SUBSTRATE BINDING (BY SIMILARITY).
FT   ACT_SITE    373    373       BASE (BY SIMILARITY).
SQ   SEQUENCE   387 AA;  40917 MW;  1690502C07AE9F63 CRC64;

  Query Match             34.4%;  Score 52;  DB 1;  Length 387;
  Best Local Similarity   60.0%;  Pred. No. 2.6;
  Matches    9;  Conservative    3;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 IVDLQRSPMGRKQGG 24
              |:|  |:|||| :||
Db          6 IIDAVRTPMGRSKGG 20


RESULT 11
OXAA_PROMI
ID   OXAA_PROMI     STANDARD;      PRT;   237 AA.
AC   P22833;
DT   01-AUG-1991 (Rel. 19, Created)
DT   01-AUG-1991 (Rel. 19, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Inner membrane protein oxaA (Fragment).
GN   OXAA.
OS   Proteus mirabilis.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Proteus.
OX   NCBI_TaxID=584;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=LM1509;
RX   MEDLINE=91033012; PubMed=2172087;
RA   Skovgaard O.;
RT   "Nucleotide sequence of a Proteus mirabilis DNA fragment homologous to
RT   the 60K-rnpA-rpmH-dnaA-dnaN-recF-gyrB region of Escherichia coli.";
RL   Gene 93:27-34(1990).
CC   -!- FUNCTION: Required for the insertion of integral membrane proteins
CC       into the membrane. Probably plays an essential role in the
CC       integration of proteins of the respiratory chain complexes.
CC       Involved in integration of membrane proteins that insert
CC       dependently and independently of the Sec translocase complex (By
CC       similarity).
CC   -!- SUBUNIT: Specifically interacts with transmembrane segments of
CC       nascent integral membrane proteins during membrane integration (By
CC       similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC       (By similarity).
CC   -!- SIMILARITY: Belongs to the OXA1/oxaA family. Subfamily 1.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; M58352; AAA83954.1; -.
DR   PIR; JQ0729; JQ0729.
DR   HAMAP; MF_01810; -; 1.
DR   InterPro; IPR001708; 60kDa_innermeb.
DR   PRINTS; PR00701; 60KDINNERMP.
KW   Transmembrane; Inner membrane.
FT   TRANSMEM      7     23       POTENTIAL.
FT   NON_TER     237    237
SQ   SEQUENCE   237 AA;  26664 MW;  07FCC405B9DB3F36 CRC64;

  Query Match             33.8%;  Score 51;  DB 1;  Length 237;
  Best Local Similarity   31.0%;  Pred. No. 2.2;
  Matches    9;  Conservative   12;  Mismatches    4;  Indels    4;  Gaps    1;

Qy          2 RMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ::: ::||::||: :     ||||:|: :
Db         61 KLITVKTDVLDLRIN----TQGGTIDEAD 85


RESULT 12
ACSA_SYNEL
ID   ACSA_SYNEL     STANDARD;      PRT;   656 AA.
AC   Q8DKH2;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Acetyl-coenzyme A synthetase (EC 6.2.1.1) (Acetate--CoA ligase) (Acyl-
DE   activating enzyme).
GN   ACSA OR TLL0887.
OS   Synechococcus elongatus (Thermosynechococcus elongatus).
OC   Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
OX   NCBI_TaxID=32046;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BP-1;
RX   MEDLINE=22225144; PubMed=12240834;
RA   Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA   Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
RA   Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA   Shimpo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RT   "Complete genome structure of the thermophilic cyanobacterium
RT   Thermosynechococcus elongatus BP-1.";
RL   DNA Res. 9:123-130(2002).
CC   -!- CATALYTIC ACTIVITY: ATP + acetate + CoA = AMP + diphosphate +
CC       acetyl-CoA.
CC   -!- PTM: Acetylated. Deacetylation by the SIR2-homolog deacetylase
CC       activates the enzyme (By similarity).
CC   -!- SIMILARITY: Belongs to the ATP-dependent AMP-binding enzyme
CC       family.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; AP005372; BAC08439.1; -.
DR   HAMAP; MF_01123; -; 1.
DR   InterPro; IPR000873; AMP-bind.
DR   Pfam; PF00501; AMP-binding; 1.
DR   PRINTS; PR00154; AMPBINDING.
DR   PROSITE; PS00455; AMP_BINDING; 1.
KW   Ligase; Acetylation; Complete proteome.
FT   ACT_SITE    529    529       BY SIMILARITY.
FT   MOD_RES     621    621       ACETYLATION (BY SIMILARITY).
SQ   SEQUENCE   656 AA;  73164 MW;  73462DCAF43F8ED2 CRC64;

  Query Match             33.8%;  Score 51;  DB 1;  Length 656;
  Best Local Similarity   50.0%;  Pred. No. 6.6;
  Matches    9;  Conservative    5;  Mismatches    4;  Indels    0;  Gaps    0;

Qy          9 DIVDLQRSPMGRKQGGTL 26
              |:|||: :|:|  :|| |
Db        454 DVVDLEGNPVGVNEGGYL 471


RESULT 13
IF2_CHLCV
ID   IF2_CHLCV      STANDARD;      PRT;   887 AA.
AC   Q823F2;
DT   10-OCT-2003 (Rel. 42, Created)
DT   10-OCT-2003 (Rel. 42, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Translation initiation factor IF-2.
GN   INFB OR CCA00465.
OS   Chlamydophila caviae.
OC   Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX   NCBI_TaxID=83557;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=GPIC;
RX   MEDLINE=22569155; PubMed=12682364;
RA   Read T.D., Myers G.S.A., Brunham R.C., Nelson W.C., Paulsen I.T.,
RA   Heidelberg J., Holtzapple E., Khouri H., Federova N.B., Carty H.A.,
RA   Umayam L.A., Haft D.H., Peterson J., Beanan M.J., White O.,
RA   Salzberg S.L., Hsia R.-C., McClarty G., Rank R.G., Bavoil P.M.,
RA   Fraser C.M.;
RT   "Genome sequence of Chlamydophila caviae (Chlamydia psittaci GPIC):
RT   examining the role of niche-specific genes in the evolution of the
RT   Chlamydiaceae.";
RL   Nucleic Acids Res. 31:2134-2147(2003).
CC   -!- FUNCTION: One of the essential components for the initiation of
CC       protein synthesis. Protects formylmethionyl-tRNA from spontaneous
CC       hydrolysis and promotes its binding to the 30S ribosomal subunits.
CC       Also involved in the hydrolysis of GTP during the formation of the
CC       70S ribosomal complex (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: Belongs to the IF-2 family.
CC   ---------------------------------------------------------------------------
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CC   ---------------------------------------------------------------------------
DR   EMBL; AE016995; AAP05210.1; -.
DR   TIGR; CCA00465; -.
DR   HAMAP; MF_00100; -; 1.
DR   InterPro; IPR000795; EF_GTPbind.
DR   InterPro; IPR004161; EFTU_D2.
DR   InterPro; IPR000178; IF2.
DR   InterPro; IPR006847; IF2_N.
DR   InterPro; IPR005225; Small_GTP.
DR   InterPro; IPR009000; Translat_factor.
DR   Pfam; PF00009; GTP_EFTU; 1.
DR   Pfam; PF03144; GTP_EFTU_D2; 2.
DR   Pfam; PF04760; IF2_N; 1.
DR   ProDom; PD186100; IF2; 1.
DR   TIGRFAMs; TIGR00487; IF-2; 1.
DR   TIGRFAMs; TIGR00231; small_GTP; 1.
DR   PROSITE; PS01176; IF2; 1.
KW   Initiation factor; Protein biosynthesis; GTP-binding;
KW   Complete proteome.
FT   DOMAIN      396    544       G-DOMAIN.
FT   NP_BIND     402    409       GTP (BY SIMILARITY).
FT   NP_BIND     448    452       GTP (BY SIMILARITY).
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FT   NP_BIND     502    505       GTP (BY SIMILARITY).
SQ   SEQUENCE   887 AA;  96938 MW;  F13EECD1700CF6B7 CRC64;

  Query Match             33.1%;  Score 50;  DB 1;  Length 887;
  Best Local Similarity   38.1%;  Pred. No. 13;
  Matches    8;  Conservative    8;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          3 MMALQTDIVDLQRSPMGRKQG 23
              |:||| :::::|: :|   | :|
Db        551 MLALQAEVLELKANPSARARG 571


RESULT 14
IF2_CHLPN
ID   IF2_CHLPN      STANDARD;      PRT;   890 AA.
AC   Q9Z8M1; Q9JRX1;
DT   30-MAY-2000 (Rel. 39, Created)
DT   16-OCT-2001 (Rel. 40, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Translation initiation factor IF-2.
GN   INFB OR CPN0317 OR CP0440 OR CPB0327.
OS   Chlamydia pneumoniae (Chlamydophila pneumoniae).
OC   Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydophila.
OX   NCBI_TaxID=83558;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=CWL029;
RX   MEDLINE=99206606; PubMed=10192388;
RA   Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W.,
RA   Olinger L., Grimwood J., Davis R.W., Stephens R.S.;
RT   "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
RL   Nat. Genet. 21:385-389(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=AR39;
RX   MEDLINE=20150255; PubMed=10684935;
RA   Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA   White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA   Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA   Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA   Eisen J., Fraser C.M.;
RT   "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT   pneumoniae AR39.";
RL   Nucleic Acids Res. 28:1397-1406(2000).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=J138;
RX   MEDLINE=20330349; PubMed=10871362;
RA   Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Ouchi K.,
RA   Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.;
RT   "Comparison of whole genome sequences of Chlamydia pneumoniae J138
RT   from Japan and CWL029 from USA.";
RL   Nucleic Acids Res. 28:2311-2314(2000).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   STRAIN=TW-183;
RA   Geng M.M., Schuhmacher A., Muehldorfer I., Bensch K.W., Schaefer K.P.,
RA   Schneider S., Pohl T., Essig A., Marre R., Melchers K.;
RT   "The genome sequence of Chlamydia pneumoniae TW183 and comparison with
RT   other Chlamydia strains based on whole genome sequence analysis.";
RL   Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: One of the essential components for the initiation of
CC       protein synthesis. Protects formylmethionyl-tRNA from spontaneous
CC       hydrolysis and promotes its binding to the 30S ribosomal subunits.
CC       Also involved in the hydrolysis of GTP during the formation of the
CC       70S ribosomal complex (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: Belongs to the IF-2 family.
CC   ---------------------------------------------------------------------
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CC   ---------------------------------------------------------------------
DR   EMBL; AE001616; AAD18466.1; -.
DR   EMBL; AE002205; AAF38279.1; -.
DR   EMBL; AP002546; BAA98527.1; -.
DR   EMBL; AE017158; AAP98260.1; ALT_INIT.
DR   PIR; E81576; E81576.
DR   PIR; E86530; E86530.
DR   PIR; F72093; F72093.
DR   TIGR; CP0440; -.
DR   HAMAP; MF_00100; -; 1.
DR   InterPro; IPR000795; EF_GTPbind.
DR   InterPro; IPR004161; EFTU_D2.
DR   InterPro; IPR000178; IF2.
DR   InterPro; IPR006847; IF2_N.
DR   InterPro; IPR005225; Small_GTP.
DR   InterPro; IPR009000; Translat_factor.
DR   Pfam; PF00009; GTP_EFTU; 1.
DR   Pfam; PF03144; GTP_EFTU_D2; 2.
DR   Pfam; PF04760; IF2_N; 1.
DR   ProDom; PD186100; IF2; 1.
DR   TIGRFAMs; TIGR00487; IF-2; 1.
DR   TIGRFAMs; TIGR00231; small_GTP; 1.
DR   PROSITE; PS01176; IF2; 1.
KW   Initiation factor; Protein biosynthesis; GTP-binding;
KW   Complete proteome.
FT   DOMAIN      398    546       G-DOMAIN.
FT   NP_BIND     404    411       GTP (BY SIMILARITY).
FT   NP_BIND     450    454       GTP (BY SIMILARITY).
FT   NP_BIND     504    507       GTP (BY SIMILARITY).
FT   VARIANT     321    321       T -> A (in strains CWL029 and TW-183).
SQ   SEQUENCE   890 AA;  97104 MW;  BBB4C2C269268781 CRC64;

  Query Match             32.5%;  Score 49;  DB 1;  Length 890;
  Best Local Similarity   38.1%;  Pred. No. 19;
  Matches    8;  Conservative    7;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          3 MMALQTDIVDLQRSPMGRKQG 23
              |:||| :::::|:  |   | :|
Db        553 MLALQAEVLELKADPSARARG 573


RESULT 15
IF2_CHLTR
ID   IF2_CHLTR      STANDARD;      PRT;   892 AA.
AC   O84098;
DT   30-MAY-2000 (Rel. 39, Created)
DT   30-MAY-2000 (Rel. 39, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Translation initiation factor IF-2.
GN   INFB OR CT096.
OS   Chlamydia trachomatis.
OC   Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX   NCBI_TaxID=813;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=D/UW-3/Cx;
RX   MEDLINE=99000809; PubMed=9784136;
RA   Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L.,
RA   Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA   Davis R.W.;
RT   "Genome sequence of an obligate intracellular pathogen of humans:
RT   Chlamydia trachomatis.";
RL   Science 282:754-759(1998).
CC   -!- FUNCTION: One of the essential components for the initiation of
CC       protein synthesis. Protects formylmethionyl-tRNA from spontaneous
CC       hydrolysis and promotes its binding to the 30S ribosomal subunits.
CC       Also involved in the hydrolysis of GTP during the formation of the
CC       70S ribosomal complex (By similarity).
CC   -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC   -!- SIMILARITY: Belongs to the IF-2 family.
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CC   ----------------------------------------------------------------------
DR   EMBL; AE001283; AAC67687.1; -.
DR   PIR; H71558; H71558.
DR   HAMAP; MF_00100; -; 1.
DR   InterPro; IPR000795; EF_GTPbind.
DR   InterPro; IPR004161; EFTU_D2.
DR   InterPro; IPR000178; IF2.
DR   InterPro; IPR006847; IF2_N.
DR   InterPro; IPR005225; Small_GTP.
DR   InterPro; IPR009000; Translat_factor.
DR   Pfam; PF00009; GTP_EFTU; 1.
DR   Pfam; PF03144; GTP_EFTU_D2; 2.
DR   Pfam; PF04760; IF2_N; 1.
DR   ProDom; PD186100; IF2; 1.
DR   TIGRFAMs; TIGR00487; IF-2; 1.
DR   TIGRFAMs; TIGR00231; small_GTP; 1.
DR   PROSITE; PS01176; IF2; 1.
KW   Initiation factor; Protein biosynthesis; GTP-binding;
KW   Complete proteome.
FT   DOMAIN      400    548       G-DOMAIN.
FT   NP_BIND     406    413       GTP (BY SIMILARITY).
FT   NP_BIND     452    456       GTP (BY SIMILARITY).
FT   NP_BIND     506    509       GTP (BY SIMILARITY).
SQ   SEQUENCE   892 AA;  97009 MW;  9D401C079D6B1A51 CRC64;

  Query Match             32.5%;  Score 49;  DB 1;  Length 892;
  Best Local Similarity   38.1%;  Pred. No. 19;
  Matches    8;  Conservative    7;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          3 MMALQTDIVDLQRSPMGRKQG 23
              |:||| ::::|:  |  | :|
Db        555 MLALQAEVLELKADPSARARG 575


Search completed: September 24, 2004, 09:43:34
Job time : 25 secs
```

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 24, 2004, 09:40:58 ; Search time 116 Seconds
(without alignments)
81.600 Million cell updates/sec

Title: US-09-806-701-16_COPY_331_360
Perfect score: 151
Sequence: 1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL_25:*
1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	151	100.0	756	6	Q95KV0	Q95kv0 bos taurus
2	84	55.6	584	11	Q80VU2	Q80vu2 mus musculu
3	84	55.6	740	6	Q95KV1	Q95kv1 bos taurus
4	84	55.6	745	11	Q8CBT3	Q8cbt3 mus musculu
5	83	55.0	758	13	Q7ZTU1	Q7ztu1 brachydanio
6	66.5	44.0	732	5	O61565	O61565 crassostrea
7	56	37.1	465	2	Q9APZ1	Q9apz1 pseudomonas
8	56	37.1	465	16	Q88DF2	Q88df2 pseudomonas
9	55	36.4	283	2	Q9X6F2	Q9x6f2 pseudomonas
10	55	36.4	283	16	Q9HUL1	Q9hul1 pseudomonas
11	55	36.4	283	16	Q87VI3	Q87vi3 pseudomonas
12	55	36.4	533	10	Q9ZRX1	Q9zrx1 glycine max
13	54	35.8	387	16	Q8FBI3	Q8fbi3 escherichia
14	54	35.8	387	16	Q83PG2	Q83pg2 shigella fl
15	54	35.8	391	2	Q93Q11	Q93q11 pseudomonas
16	54	35.8	391	2	Q9R9W0	Q9r9w0 pseudomonas
17	54	35.8	391	16	Q9HZJ3	Q9hzj3 pseudomonas
18	54	35.8	391	16	Q88L01	Q88l01 pseudomonas
19	54	35.8	391	16	Q87ZB3	Q87zb3 pseudomonas
20	53.5	35.4	1710	5	Q9V9N7	Q9v9n7 drosophila
21	53	35.1	387	16	Q9KNI0	Q9kni0 vibrio chol
22	53	35.1	387	16	Q8DDK5	Q8ddk5 vibrio vuln
23	52.5	34.8	649	10	Q9AW00	Q9aw00 guillardia
24	52	34.4	387	2	Q9F0Y6	Q9f0y6 enterobacte
25	52	34.4	391	16	Q87TP0	Q87tp0 vibrio para
26	51	33.8	174	10	Q7XBP1	Q7xbp1 chlorarachn
27	51	33.8	396	16	Q93JG7	Q93jg7 streptomyce
28	50.5	33.4	617	13	Q9PU64	Q9pu64 brachydanio
29	50.5	33.4	617	13	Q9IAA9	Q9iaa9 brachydanio
30	50.5	33.4	617	13	Q804R6	Q804r6 brachydanio
31	50.5	33.4	4317	16	Q88F56	Q88f56 pseudomonas
32	50	33.1	465	16	Q82XR0	Q82xr0 nitrosomona
33	49.5	32.8	297	16	Q9KE47	Q9ke47 bacillus ha
34	49	32.5	242	16	Q88IZ8	Q88iz8 pseudomonas
35	49	32.5	301	16	Q8DUQ1	Q8duq1 streptococc
36	49	32.5	401	16	Q7VVB8	Q7vvb8 bordetella
37	49	32.5	494	16	Q8F3M2	Q8f3m2 leptospira
38	49	32.5	536	10	Q8L994	Q8l994 arabidopsis
39	49	32.5	536	10	Q9LV21	Q9lv21 arabidopsis
40	49	32.5	676	2	O07365	O07365 chlamydia t
41	48.5	32.1	304	16	Q81MD1	Q81md1 bacillus an
42	48.5	32.1	304	16	Q818Z0	Q818z0 bacillus ce
43	48.5	32.1	351	2	Q8GII9	Q8gii9 gamma-prote
44	48.5	32.1	373	16	Q9I140	Q9i140 pseudomonas
45	48.5	32.1	373	16	Q88P67	Q88p67 pseudomonas

ALIGNMENTS

RESULT 1
Q95KV0
ID Q95KV0 PRELIMINARY; PRT; 756 AA.
AC Q95KV0;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE IkB kinase-beta.
GN BIKKBETA.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;
RT "Identification and characterisation of the bovine IkB kinases (IKKs)
RT alpha, beta and gamma.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL; AJ414556; CAC93687.1; -.
DR GO; GO:0005524; F:ATP binding; IEA.
DR GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR GO; GO:0016740; F:transferase activity; IEA.
DR GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR InterPro; IPR000719; Prot_kinase.
DR InterPro; IPR008271; Ser_thr_pkin_AS.
DR InterPro; IPR001245; Tyr_pkinase.
DR Pfam; PF00069; pkinase; 1.
DR PRINTS; PR00109; TYRKINASE.
DR ProDom; PD000001; Prot_kinase; 1.
DR PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ SEQUENCE 756 AA; 86647 MW; A072D15614A176E5 CRC64;

Query Match 100.0%; Score 151; DB 6; Length 756;

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  Best Local Similarity   100.0%;  Pred. No. 1.1e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ||||||||||||||||||||||||||||||
Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


RESULT 2
Q80VU2
ID   Q80VU2      PRELIMINARY;      PRT;   584 AA.
AC   Q80VU2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Conserved helix-loop-helix ubiquitous kinase.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye;
RA   Strausberg R.;
RL   Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC018243; AAH18243.1; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   Kinase.
SQ   SEQUENCE   584 AA;  66805 MW;  D99BB8A6DF1CA4EB CRC64;

  Query Match             55.6%;  Score 84;  DB 11;  Length 584;
  Best Local Similarity   46.7%;  Pred. No. 0.00024;
  Matches   14;  Conservative   11;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              :::|:| |:|::||:|| ||:||  :: ||
Db        532 DQIMSLHTEIMELQKSPYGRRQGDLMESLE 561


RESULT 3
Q95KV1
ID   Q95KV1      PRELIMINARY;      PRT;   740 AA.
AC   Q95KV1;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   IkB kinase-alpha.
GN   BIKKALPHA.
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC   Bovidae; Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Rottenberg S., Dobbelaere D.A.E., Heussler V.T.;
RT   "Identification and characterisation of the bovine IkB kinases (IKKs)
RT   alpha, beta and gamma.";
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR   EMBL; AJ414555; CAC93686.1; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   740 AA;  84343 MW;  01903BE11F44D176 CRC64;

  Query Match             55.6%;  Score 84;  DB 6;  Length 740;
  Best Local Similarity   46.7%;  Pred. No. 0.00032;
  Matches   14;  Conservative   11;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              :::|:| |:|::||:|| ||:||  :: ||
Db        532 DQIMSLHTEIMELQKSPYGRRQGDLMESLE 561


RESULT 4
Q8CBT3
ID   Q8CBT3      PRELIMINARY;      PRT;   745 AA.
AC   Q8CBT3;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Conserved helix-loop-helix ubiquitous kinase.
GN   CHUK.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Urinary bladder;
RX   MEDLINE=22354683; PubMed=12466851;
RA   The FANTOM Consortium,
RA   the RIKEN Genome Exploration Research Group Phase I & II Team;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
DR   EMBL; AK035326; BAC29034.1; -.
DR   MGD; MGI:99484; Chuk.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
SQ   SEQUENCE   745 AA;  84770 MW;  48C9E01C17A61184 CRC64;
```

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  Query Match           55.6%;  Score 84;  DB 11;  Length 745;
  Best Local Similarity  46.7%;  Pred. No. 0.00032;
  Matches   14;  Conservative   11;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              :::|:| |:|::||:|| ||:||  :: ||
Db        532 DQIMSLHTEIMELQKSPYGRRQGDLMESLE 561


RESULT 5
Q7ZTU1
ID   Q7ZTU1      PRELIMINARY;      PRT;   758 AA.
AC   Q7ZTU1;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Hypothetical protein.
OS   Brachydanio rerio (Zebrafish) (Danio rerio).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC   Cyprinidae; Danio.
OX   NCBI_TaxID=7955;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Body;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA   Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA   Jones S.J., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Body;
RA   Strausberg R.;
RL   Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; BC051614; AAH51614.1; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR002290; Ser_thr_pkinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   SMART; SM00220; S_TKc; 1.
DR   SMART; SM00219; TyrKc; 1.
DR   PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   Hypothetical protein.
SQ   SEQUENCE   758 AA;  87187 MW;  6001AADA3F74A432 CRC64;

  Query Match           55.0%;  Score 83;  DB 13;  Length 758;
  Best Local Similarity  50.0%;  Pred. No. 0.00047;
  Matches   15;  Conservative    8;  Mismatches    7;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              | :||| ::||:|||||  |:||  :: |:
Db        533 EEIMALHSEIVELQRSPYARRQGDVMEQLQ 562


RESULT 6
O61565
ID   O61565      PRELIMINARY;      PRT;   732 AA.
AC   O61565;
DT   01-AUG-1998 (TrEMBLrel. 07, Created)
DT   01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   I-kappa-B kinase.
GN   IKK.
OS   Crassostrea gigas (Pacific oyster).
OC   Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Ostreoida;
OC   Ostreoidea; Ostreidae; Crassostrea.
OX   NCBI_TaxID=29159;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=99332074; PubMed=10405163;
RA   Escoubas J.M., Briant L., Montagnani C., Hez S., Devaux C., Roch P.;
RT   "Oyster IKK-like protein shares structural and functional properties
RT   with its mammalian homologues.";
RL   FEBS Lett. 453:293-298(1999).
CC   -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR   EMBL; AF051320; AAC05683.1; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004674; F:protein serine/threonine kinase activity; IEA.
DR   GO; GO:0004713; F:protein-tyrosine kinase activity; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0006468; P:protein amino acid phosphorylation; IEA.
DR   InterPro; IPR000719; Prot_kinase.
DR   InterPro; IPR008271; Ser_thr_pkin_AS.
DR   InterPro; IPR001245; Tyr_pkinase.
DR   Pfam; PF00069; pkinase; 1.
DR   PRINTS; PR00109; TYRKINASE.
DR   ProDom; PD000001; Prot_kinase; 1.
DR   PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
DR   PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
KW   ATP-binding; Kinase; Serine/threonine-protein kinase; Transferase.
SQ   SEQUENCE   732 AA;  84215 MW;  871EE8D1CA3E39AF CRC64;

  Query Match           44.0%;  Score 66.5;  DB 5;  Length 732;
  Best Local Similarity  48.4%;  Pred. No. 0.17;
  Matches   15;  Conservative    8;  Mismatches    7;  Indels    1;  Gaps    1;

Qy          1 ERMMALQTDIVDLQRSPMGR-KQGGTLDDLE 30
              :: :|||| |::||:||  | ||   |::||
Db        528 QQSLALQTKILELQKSPFARTKQHEVLENLE 558


RESULT 7
Q9APZ1
ID   Q9APZ1      PRELIMINARY;      PRT;   465 AA.
AC   Q9APZ1;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Replicative DNA helicase DnaB.
GN   DNAB.
OS   Pseudomonas putida.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=303;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=mt2;
RX   MEDLINE=21299384; PubMed=11406602;
RA   Caspi R., Pacek M., Consiglieri G., Helinski D.R., Toukdarian A.,
RA   Konieczny I.;
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RT   "A broad host range replicon with different requirements for
RT   replication initiation in three bacterial species.";
RL   EMBO J. 20:3262-3271(2001).
DR   EMBL; AF229444; AAK00231.1; -.
DR   HSSP; P03005; 1JWE.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003678; F:DNA helicase activity; IEA.
DR   GO; GO:0000166; F:nucleotide binding; IEA.
DR   GO; GO:0006260; P:DNA replication; IEA.
DR   InterPro; IPR003593; AAA_ATPase.
DR   InterPro; IPR007694; DnaB_C.
DR   InterPro; IPR007692; DnaB_helicase.
DR   InterPro; IPR007693; DnaB_N.
DR   Pfam; PF00772; DnaB; 1.
DR   Pfam; PF03796; DnaB_C; 1.
DR   ProDom; PD332834; DnaB_C; 1.
DR   SMART; SM00382; AAA; 1.
DR   TIGRFAMs; TIGR00665; DnaB; 1.
KW   ATP-binding; Helicase.
SQ   SEQUENCE   465 AA;  51581 MW;  43A505CB32C20193 CRC64;

  Query Match             37.1%;  Score 56;  DB 2;  Length 465;
  Best Local Similarity   37.9%;  Pred. No. 4.5;
  Matches   11;  Conservative    6;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          2 RMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ::::: ||| |   :| ||     ||| |
Db        127 QLISISTDIADNAFNPQGRNAAEILDDAE 155


RESULT 8
Q88DF2
ID   Q88DF2      PRELIMINARY;      PRT;   465 AA.
AC   Q88DF2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Replicative DNA helicase.
GN   DNAB OR PP4873.
OS   Pseudomonas putida (strain KT2440).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=160488;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=22423060; PubMed=12534463;
RA   Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA   Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA   Brinkac L., Beanan M., DeBoy R.T., Daugherty S., Kolonay J.,
RA   Madupu R., Nelson W., White O., Peterson J., Khouri H., Hance I.,
RA   Chris Lee P., Holtzapple E., Scanlan D., Tran K., Moazzez A.,
RA   Utterback T., Rizzo M., Lee K., Kosack D., Moestl D., Wedler H.,
RA   Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA   Kiewitz C., Eisen J., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA   Fraser C.M.;
RT   "Complete genome sequence and comparative analysis of the
RT   metabolically versatile Pseudomonas putida KT2440.";
RL   Environ. Microbiol. 4:799-808(2002).
DR   EMBL; AE016792; AAN70442.1; -.
DR   TIGR; PP4873; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003678; F:DNA helicase activity; IEA.
DR   GO; GO:0006260; P:DNA replication; IEA.
DR   InterPro; IPR007694; DnaB_C.
DR   InterPro; IPR007693; DnaB_N.
DR   Pfam; PF00772; DnaB; 1.
DR   Pfam; PF03796; DnaB_C; 1.
KW   Helicase; Complete proteome.
SQ   SEQUENCE   465 AA;  51581 MW;  43A505CB32C20193 CRC64;

  Query Match             37.1%;  Score 56;  DB 16;  Length 465;
  Best Local Similarity   37.9%;  Pred. No. 4.5;
  Matches   11;  Conservative    6;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          2 RMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ::::: ||| |   :| ||     ||| |
Db        127 QLISISTDIADNAFNPQGRNAAEILDDAE 155


RESULT 9
Q9X6F2
ID   Q9X6F2      PRELIMINARY;      PRT;   283 AA.
AC   Q9X6F2;
DT   01-NOV-1999 (TrEMBLrel. 12, Created)
DT   01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT   01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE   RpmA.
GN   RPMA.
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=287;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=4020;
RX   MEDLINE=20231781; PubMed=10768936;
RA   Simpson D.A., Speert D.P.;
RT   "RpmA is required for nonopsonic phagocytosis of Pseudomonas
RT   aeruginosa.";
RL   Infect. Immun. 68:2493-2502(2000).
DR   EMBL; AF136403; AAD33690.1; -.
SQ   SEQUENCE   283 AA;  30740 MW;  4AA5DAC6957C0693 CRC64;

  Query Match             36.4%;  Score 55;  DB 2;  Length 283;
  Best Local Similarity   46.4%;  Pred. No. 3.6;
  Matches   13;  Conservative    3;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDD 28
              | |||:: || |   ||:  |  | | |
Db         91 EGMMAIEADIEDPAASPIFSKYPGVLKD 118


RESULT 10
Q9HUL1
ID   Q9HUL1      PRELIMINARY;      PRT;   283 AA.
AC   Q9HUL1;
DT   01-MAR-2001 (TrEMBLrel. 16, Created)
DT   01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Chemotaxis protein MotA.
GN   MOTA OR PA4954.
OS   Pseudomonas aeruginosa.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=287;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC 15692 / PAO1;
RX   MEDLINE=20437337; PubMed=10984043;
RA   Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,
RA   Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA   Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA   Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA   Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA   Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT   "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT   opportunistic pathogen.";
RL   Nature 406:959-964(2000).
DR   EMBL; AE004908; AAG08339.1; -.
DR   PIR; H83026; H83026.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0003774; F:motor activity; IEA.
DR   GO; GO:0008565; F:protein transporter activity; IEA.
DR   GO; GO:0006935; P:chemotaxis; IEA.
DR   GO; GO:0001539; P:ciliary/flagellar motility; IEA.
DR   GO; GO:0006810; P:transport; IEA.
```

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DR   InterPro; IPR000540; Flag_MotA.
DR   InterPro; IPR002898; MotA_ExbB.
DR   Pfam; PF01618; MotA_ExbB; 1.
DR   PROSITE; PS01307; MOTA; 1.
KW   Complete proteome.
SQ   SEQUENCE   283 AA;  30094 MW;  9741C163CC63687B CRC64;

  Query Match             36.4%;  Score 55;  DB 16;  Length 283;
  Best Local Similarity   46.4%;  Pred. No. 3.6;
  Matches   13;  Conservative    3;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDD 28
              | |||:: || |   ||:  |  | | |
Db         91 EGMMAIEADIEDPAASPIFSKYPGVLKD 118


RESULT 11
Q87VI3
ID   Q87VI3      PRELIMINARY;      PRT;   283 AA.
AC   Q87VI3;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Chemotaxis motA protein.
GN   MOTA-2 OR PSPTO4953.
OS   Pseudomonas syringae (pv. tomato).
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=323;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=DC3000;
RA   Buell R., Joardar V., Khouri H., Fedorova N., Tran B., Russell D.,
RA   Berry K., Utterback T., Van Aken S., Feldblyum T., Gwinn M.,
RA   Dodson R., DeBoy R., Durkin A., Kolonay J., Madupu R., Daugherty S.,
RA   Brinkac L., Beanan M., Haft D., Selengut J., Nelson W., Davidsen T.,
RA   White O., Fraser C., Collmer A.;
RT   "Complete sequence of Pseudomonas syringae.";
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AE016873; AAO58381.1; -.
DR   TIGR; PSPTO4953; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0003774; F:motor activity; IEA.
DR   GO; GO:0006935; P:chemotaxis; IEA.
DR   GO; GO:0001539; P:ciliary/flagellar motility; IEA.
DR   InterPro; IPR000540; Flag_MotA.
DR   PROSITE; PS01307; MOTA; 1.
KW   Complete proteome.
SQ   SEQUENCE   283 AA;  30393 MW;  C6340C897E4D03C7 CRC64;

  Query Match             36.4%;  Score 55;  DB 16;  Length 283;
  Best Local Similarity   46.4%;  Pred. No. 3.6;
  Matches   13;  Conservative    3;  Mismatches   12;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDD 28
              | |||:: || |   ||:  |  | | |
Db         91 EGMMAIEGDIEDAASSPIFAKYPGVLKD 118


RESULT 12
Q9ZRX1
ID   Q9ZRX1      PRELIMINARY;      PRT;   533 AA.
AC   Q9ZRX1;
DT   01-MAY-1999 (TrEMBLrel. 10, Created)
DT   01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Cytosolic chaperonin, delta-subunit.
GN   CCTD.
OS   Glycine max (Soybean).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC   eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
OX   NCBI_TaxID=3847;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=cv. M103;
RA   Tran Thi Phuong L., Nguyen Huy H., Chu Hoang H., Dinh Duy K.,
RA   Nong Van H., Le Thi M.;
RT   "Cloning of a cytosolic chaperonin gene from high-temperature tolerant
RT   soybean cultivar M103.";
RL   Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AJ012318; CAA09989.1; -.
DR   HSSP; P48424; 1A6D.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0003754; F:chaperone activity; IEA.
DR   InterPro; IPR002194; Chaperonin_TCP-1.
DR   InterPro; IPR001844; Chaprnin_Cpn60.
DR   InterPro; IPR002423; Cpn60/TCP-1.
DR   InterPro; IPR008950; GroEL-ATPase.
DR   InterPro; IPR001092; HLH_basic.
DR   Pfam; PF00118; cpn60_TCP1; 1.
DR   PRINTS; PR00298; CHAPERONIN60.
DR   PRINTS; PR00304; TCOMPLEXTCP1.
DR   PROSITE; PS00038; HLH_1; 1.
DR   PROSITE; PS00750; TCP1_1; 1.
DR   PROSITE; PS00995; TCP1_3; 1.
KW   ATP-binding; Chaperone.
SQ   SEQUENCE   533 AA;  57573 MW;  EF4E5D2E8D190AF2 CRC64;

  Query Match             36.4%;  Score 55;  DB 10;  Length 533;
  Best Local Similarity   46.2%;  Pred. No. 7.5;
  Matches   12;  Conservative    6;  Mismatches    8;  Indels    0;  Gaps    0;

Qy          5 ALQTDIVDLQRSPMGRKQGGTLDDLE 30
              | : |:|||:   : :| |||:|| |
Db        190 APKPDMVDLRDVKIVKKLGGTVDDTE 215


RESULT 13
Q8FBI3
ID   Q8FBI3      PRELIMINARY;      PRT;   387 AA.
AC   Q8FBI3;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   3-ketoacyl-CoA thiolase (EC 2.3.1.16).
GN   FADA OR C4792.
OS   Escherichia coli O6.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Escherichia.
OX   NCBI_TaxID=217992;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=O6:H1 / CFT073 / ATCC 700928;
RX   MEDLINE=22388234; PubMed=12471157;
RA   Welch R.A., Burland V., Plunkett G. III, Redford P., Roesch P.,
RA   Rasko D., Buckles E.L., Liou S.-R., Boutin A., Hackett J., Stroud D.,
RA   Mayhew G.F., Rose D.J., Zhou S., Schwartz D.C., Perna N.T.,
RA   Mobley H.L.T., Donnenberg M.S., Blattner F.R.;
RT   "Extensive mosaic structure revealed by the complete genome sequence
RT   of uropathogenic Escherichia coli.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:17020-17024(2002).
DR   EMBL; AE016770; AAN83225.1; -.
DR   GO; GO:0003988; F:acetyl-CoA C-acyltransferase activity; IEA.
DR   GO; GO:0008415; F:acyltransferase activity; IEA.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0016740; F:transferase activity; IEA.
DR   GO; GO:0004812; F:tRNA ligase activity; IEA.
DR   GO; GO:0006418; P:amino acid activation; IEA.
DR   InterPro; IPR002155; Thiolase.
DR   InterPro; IPR001412; tRNA-synt_I.
DR   Pfam; PF00108; thiolase; 1.
DR   Pfam; PF02803; thiolase_C; 1.
DR   PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
DR   PROSITE; PS00098; THIOLASE_1; 1.
DR   PROSITE; PS00737; THIOLASE_2; 1.
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DR   PROSITE; PS00099; THIOLASE_3; 1.
KW   Acyltransferase; Transferase; Complete proteome.
SQ   SEQUENCE   387 AA;  40775 MW;  505E4A821C40C007 CRC64;

  Query Match             35.8%;  Score 54;  DB 16;  Length 387;
  Best Local Similarity   61.1%;  Pred. No. 7.5;
  Matches   11;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          7 QTDIVDLQRSPMGRKQGG 24
              |  |||  |:|||| :||
Db          3 QVVIVDAIRTPMGRSKGG 20


RESULT 14
Q83PG2
ID   Q83PG2      PRELIMINARY;      PRT;   387 AA.
AC   Q83PG2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Fatty acid oxidizing complex (Thiolase I, 3-ketoacyl-CoA thiolase,
DE   acetyl-CoA transferase).
GN   FADA OR SF3921 OR S3831.
OS   Shigella flexneri.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC   Enterobacteriaceae; Shigella.
OX   NCBI_TaxID=623;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=301 / Serotype 2a;
RX   MEDLINE=22272406; PubMed=12384590;
RA   Jin Q., Yuan Z., Xu J., Wang Y., Shen Y., Lu W., Wang J., Liu H.,
RA   Yang J., Yang F., Zhang X., Zhang J., Yang G., Wu H., Qu D., Dong J.,
RA   Sun L., Xue Y., Zhao A., Gao Y., Zhu J., Kan B., Ding K., Chen S.,
RA   Cheng H., Yao Z., He B., Chen R., Ma D., Qiang B., Wen Y., Hou Y.,
RA   Yu J.;
RT   "Genome sequence of Shigella flexneri 2a: insights into pathogenicity
RT   through comparison with genomes of Escherichia coli K12 and O157.";
RL   Nucleic Acids Res. 30:4432-4441(2002).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=2457T / ATCC 700930 / Serotype 2a;
RX   MEDLINE=22590274; PubMed=12704152;
RA   Wei J., Goldberg M.B., Burland V., Venkatesan M.M., Deng W.,
RA   Fournier G., Mayhew G.F., Plunkett G. III, Rose D.J., Darling A.,
RA   Mau B., Perna N.T., Payne S.M., Runyen-Janecky L.J., Zhou S.,
RA   Schwartz D.C., Blattner F.R.;
RT   "Complete genome sequence and comparative genomics of Shigella
RT   flexneri serotype 2a strain 2457T.";
RL   Infect. Immun. 71:2775-2786(2003).
DR   EMBL; AE015399; AAN45356.1; -.
DR   EMBL; AE016990; AAP18842.1; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004812; F:tRNA ligase activity; IEA.
DR   GO; GO:0006418; P:amino acid activation; IEA.
DR   InterPro; IPR002155; Thiolase.
DR   InterPro; IPR001412; tRNA-synt_I.
DR   Pfam; PF00108; thiolase; 1.
DR   Pfam; PF02803; thiolase_C; 1.
DR   PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
DR   PROSITE; PS00098; THIOLASE_1; 1.
DR   PROSITE; PS00737; THIOLASE_2; 1.
DR   PROSITE; PS00099; THIOLASE_3; 1.
KW   Transferase; Complete proteome.
SQ   SEQUENCE   387 AA;  40846 MW;  AE706AE0CBC0B0F0 CRC64;

  Query Match             35.8%;  Score 54;  DB 16;  Length 387;
  Best Local Similarity   61.1%;  Pred. No. 7.5;
  Matches   11;  Conservative    2;  Mismatches    5;  Indels    0;  Gaps    0;

Qy          7 QTDIVDLQRSPMGRKQGG 24
              |  |||  |:|||| :||
Db          3 QVVIVDAIRTPMGRSKGG 20


RESULT 15
Q93Q11
ID   Q93Q11      PRELIMINARY;      PRT;   391 AA.
AC   Q93Q11;
DT   01-DEC-2001 (TrEMBLrel. 19, Created)
DT   01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Beta-ketothiolase FadA.
GN   FADA.
OS   Pseudomonas oleovorans.
OC   Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC   Pseudomonadaceae; Pseudomonas.
OX   NCBI_TaxID=301;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=ATCC29347;
RA   Fiedler S., Steinbuechel A., Rehm B.H.A.;
RT   "fadBA genes from Pseudomonas oleovorans ATCC29347.";
RL   Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF288535; AAK83059.1; -.
DR   GO; GO:0005524; F:ATP binding; IEA.
DR   GO; GO:0004812; F:tRNA ligase activity; IEA.
DR   GO; GO:0006418; P:amino acid activation; IEA.
DR   InterPro; IPR002155; Thiolase.
DR   InterPro; IPR001412; tRNA-synt_I.
DR   Pfam; PF00108; thiolase; 1.
DR   Pfam; PF02803; thiolase_C; 1.
DR   PROSITE; PS00178; AA_TRNA_LIGASE_I; 1.
DR   PROSITE; PS00098; THIOLASE_1; 1.
DR   PROSITE; PS00737; THIOLASE_2; 1.
SQ   SEQUENCE   391 AA;  41645 MW;  D7CAE2F37ED170A1 CRC64;

  Query Match             35.8%;  Score 54;  DB 2;  Length 391;
  Best Local Similarity   66.7%;  Pred. No. 7.5;
  Matches   10;  Conservative    2;  Mismatches    3;  Indels    0;  Gaps    0;

Qy         10 IVDLQRSPMGRKQGG 24
              |||  |:|||| :||
Db         10 IVDFGRTPMGRSKGG 24


Search completed: September 24, 2004, 09:45:37
Job time : 119 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: September 24, 2004, 09:40:59 ; Search time 18 Seconds
(without alignments)
86.043 Million cell updates/sec

Title: US-09-806-701-16_COPY_331_360
Perfect score: 151
Sequence: 1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	151	100.0	756	2	US-08-887-518-4	Sequence 4, Appli
2	151	100.0	756	2	US-09-023-321-4	Sequence 4, Appli
3	151	100.0	756	2	US-08-890-853-2	Sequence 2, Appli
4	151	100.0	756	2	US-09-032-475-4	Sequence 4, Appli
5	151	100.0	756	2	US-09-099-125A-2	Sequence 2, Appli
6	151	100.0	756	2	US-09-099-124A-2	Sequence 2, Appli
7	151	100.0	756	3	US-09-032-476-2	Sequence 2, Appli
8	151	100.0	756	3	US-08-890-854-2	Sequence 2, Appli
9	151	100.0	756	3	US-09-023-324-2	Sequence 2, Appli
10	151	100.0	756	3	US-09-168-629-15	Sequence 15, Appl
11	151	100.0	756	3	US-08-910-820-9	Sequence 9, Appli
12	151	100.0	756	4	US-09-109-986-2	Sequence 2, Appli
13	151	100.0	756	4	US-09-844-908-9	Sequence 9, Appli
14	151	100.0	756	4	US-09-868-758-4	Sequence 4, Appli
15	84	55.6	584	3	US-09-160-483-1	Sequence 1, Appli
16	79	52.3	745	2	US-08-887-518-3	Sequence 3, Appli
17	79	52.3	745	2	US-09-023-321-3	Sequence 3, Appli
18	79	52.3	745	2	US-08-890-853-4	Sequence 4, Appli
19	79	52.3	745	2	US-09-032-475-3	Sequence 3, Appli
20	79	52.3	745	2	US-09-099-125A-4	Sequence 4, Appli
21	79	52.3	745	2	US-09-099-124A-4	Sequence 4, Appli
22	79	52.3	745	3	US-09-032-476-4	Sequence 4, Appli
23	79	52.3	745	3	US-08-890-854-4	Sequence 4, Appli
24	79	52.3	745	3	US-09-023-324-4	Sequence 4, Appli
25	79	52.3	745	3	US-09-168-629-2	Sequence 2, Appli
26	79	52.3	745	3	US-08-910-820-10	Sequence 10, Appl
27	79	52.3	745	3	US-08-810-131A-2	Sequence 2, Appli
28	79	52.3	745	4	US-09-109-986-4	Sequence 4, Appli
29	79	52.3	745	4	US-09-844-908-10	Sequence 10, Appl
30	79	52.3	745	4	US-09-868-758-3	Sequence 3, Appli
31	76	50.3	996	4	US-09-417-197-123	Sequence 123, App
32	76	50.3	997	4	US-09-417-197-121	Sequence 121, App
33	55	36.4	406	4	US-09-252-991A-32895	Sequence 32895, A
34	54	35.8	388	4	US-08-178-257-15	Sequence 15, Appl
35	54	35.8	390	4	US-09-489-039A-8065	Sequence 8065, Ap
36	54	35.8	396	4	US-09-252-991A-18619	Sequence 18619, A
37	51	33.8	551	4	US-09-543-681A-7532	Sequence 7532, Ap
38	50	33.1	735	4	US-09-252-991A-32240	Sequence 32240, A
39	49	32.5	397	4	US-09-543-681A-5675	Sequence 5675, Ap
40	49	32.5	761	4	US-09-198-452A-335	Sequence 335, App
41	48.5	32.1	374	4	US-09-252-991A-23582	Sequence 23582, A
42	48	31.8	539	3	US-08-687-590-27	Sequence 27, Appl
43	48	31.8	539	4	US-09-702-705-326	Sequence 326, App
44	48	31.8	539	4	US-09-736-457-326	Sequence 326, App
45	48	31.8	539	4	US-09-614-124B-326	Sequence 326, App

ALIGNMENTS

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RESULT 1
US-08-887-518-4
; Sequence 4, Application US/08887518
; Patent No. 5843721
;  GENERAL INFORMATION:
;    APPLICANT:  Rothe, Mike
;    APPLICANT:  Wu, Lin
;    TITLE OF INVENTION:  NIK Proteins, Nucleic Acids and Methods
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  268 BUSH STREET, SUITE 3200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/887,518
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  T97-008
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 343-4341
;      TELEFAX:  (415) 343-4342
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  756 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-887-518-4

  Query Match            100.0%;  Score 151;  DB 2;  Length 756;
  Best Local Similarity  100.0%;  Pred. No. 2.4e-16;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
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Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564
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RESULT 2
US-09-023-321-4
; Sequence 4, Application US/09023321
; Patent No. 5844073
;  GENERAL INFORMATION:
;    APPLICANT:  Rothe, Mike
;    APPLICANT:  Wu, Lin
;    TITLE OF INVENTION:  NIK Proteins, Nucleic Acids and Methods
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  268 BUSH STREET, SUITE 3200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,321
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/887,518
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  T97-008
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 343-4341
;      TELEFAX:  (415) 343-4342
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  756 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-023-321-4

  Query Match             100.0%;  Score 151;  DB 2;  Length 756;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-16;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
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Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


RESULT 3
US-08-890-853-2
; Sequence 2, Application US/08890853
; Patent No. 5851812
;  GENERAL INFORMATION:
;    APPLICANT:  Goeddel, David V.
;    APPLICANT:  Woronicz, John
;    TITLE OF INVENTION:  IKK-  Proteins, Nucleic Acids and Methods
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  268 BUSH STREET, SUITE 3200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/890,853
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  T97-006-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 343-4341
;      TELEFAX:  (415) 343-4342
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  756 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-890-853-2

  Query Match             100.0%;  Score 151;  DB 2;  Length 756;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-16;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ||||||||||||||||||||||||||||||
Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


RESULT 4
US-09-032-475-4
; Sequence 4, Application US/09032475
; Patent No. 5854003
;  GENERAL INFORMATION:
;    APPLICANT:  Rothe, Mike
;    APPLICANT:  Wu, Lin
;    TITLE OF INVENTION:  NIK Proteins, Nucleic Acids and Methods
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  268 BUSH STREET, SUITE 3200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/032,475
;      FILING DATE:
;      CLASSIFICATION:  435
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/887,518
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  T97-008
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 343-4341
;      TELEFAX:  (415) 343-4342
;  INFORMATION FOR SEQ ID NO:  4:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  756 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-032-475-4
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  Query Match             100.0%;  Score 151;  DB 2;  Length 756;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-16;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ||||||||||||||||||||||||||||||
Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


RESULT 5
US-09-099-125A-2
; Sequence 2, Application US/09099125A
; Patent No. 5916760
;  GENERAL INFORMATION:
;    APPLICANT:  Goeddel, David V.
;    APPLICANT:  Woronicz, John
;    TITLE OF INVENTION:  IKK-  Proteins, Nucleic Acids and Methods
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  268 BUSH STREET, SUITE 3200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/099,125A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/890,853
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  T97-006-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 343-4341
;      TELEFAX:  (415) 343-4342
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  756 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-099-125A-2

  Query Match             100.0%;  Score 151;  DB 2;  Length 756;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-16;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ||||||||||||||||||||||||||||||
Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


RESULT 6
US-09-099-124A-2
; Sequence 2, Application US/09099124A
; Patent No. 5939302
;  GENERAL INFORMATION:
;    APPLICANT:  Goeddel, David V.
;    APPLICANT:  Woronicz, John
;    TITLE OF INVENTION:  IKK-  Proteins, Nucleic Acids and Methods
;    NUMBER OF SEQUENCES:  4
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  268 BUSH STREET, SUITE 3200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/099,124A
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/890,853
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  T97-006-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 343-4341
;      TELEFAX:  (415) 343-4342
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  756 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-099-124A-2

  Query Match             100.0%;  Score 151;  DB 2;  Length 756;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-16;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ||||||||||||||||||||||||||||||
Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


RESULT 7
US-09-032-476-2
; Sequence 2, Application US/09032476
; Patent No. 6235492
;  GENERAL INFORMATION:
;    APPLICANT:  Rothe, Mike
;    APPLICANT:  Cao, Zhaodan
;    APPLICANT:  R gnier, Catherine
;    TITLE OF INVENTION:  IKK-' Proteins, Nucleic Acids and Methods
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  268 BUSH STREET, SUITE 3200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/032,476
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/890,854
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
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```
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  T97-006-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 343-4341
;      TELEFAX:  (415) 343-4342
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  756 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-032-476-2

  Query Match             100.0%;  Score 151;  DB 3;  Length 756;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-16;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ||||||||||||||||||||||||||||||
Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


RESULT 8
US-08-890-854-2
; Sequence 2, Application US/08890854
; Patent No. 6235512
;  GENERAL INFORMATION:
;    APPLICANT:  Rothe, Mike
;    APPLICANT:  Cao, Zhaodan
;    APPLICANT:  R gnier, Catherine
;    TITLE OF INVENTION:  IKK-` Proteins, Nucleic Acids and Methods
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  268 BUSH STREET, SUITE 3200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/890,854
;      FILING DATE:
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  T97-006-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 343-4341
;      TELEFAX:  (415) 343-4342
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  756 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-08-890-854-2

  Query Match             100.0%;  Score 151;  DB 3;  Length 756;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-16;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ||||||||||||||||||||||||||||||
Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


RESULT 9
US-09-023-324-2
; Sequence 2, Application US/09023324
; Patent No. 6235513
;  GENERAL INFORMATION:
;    APPLICANT:  Rothe, Mike
;    APPLICANT:  Cao, Zhaodan
;    APPLICANT:  R gnier, Catherine
;    TITLE OF INVENTION:  IKK-` Proteins, Nucleic Acids and Methods
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  268 BUSH STREET, SUITE 3200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/023,324
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/890,854
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  T97-006-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 343-4341
;      TELEFAX:  (415) 343-4342
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  756 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-023-324-2

  Query Match             100.0%;  Score 151;  DB 3;  Length 756;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-16;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ||||||||||||||||||||||||||||||
Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


RESULT 10
US-09-168-629-15
; Sequence 15, Application US/09168629
; Patent No. 6242253
; GENERAL INFORMATION:
;  APPLICANT: Karin, Michael
;  APPLICANT: DiDonato, Joseph A.
;  APPLICANT: Rothwarf, David M.
;  APPLICANT: Hayakawa, Makio
;  APPLICANT: Zandi, Ebrahim
;  TITLE OF INVENTION: IkB Kinase, Subunits Thereof, and Methods of Using Same
;  FILE REFERENCE: P-UD 3295
;  CURRENT APPLICATION NUMBER: US/09/168,629
;  CURRENT FILING DATE: 1998-10-08
;  EARLIER APPLICATION NUMBER: 60/061,470
;  EARLIER FILING DATE: 1997-10-09
;  NUMBER OF SEQ ID NOS: 20
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;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 756
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-168-629-15

  Query Match             100.0%;  Score 151;  DB 3;  Length 756;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-16;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ||||||||||||||||||||||||||||||
Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


RESULT 11
US-08-910-820-9
; Sequence 9, Application US/08910820
; Patent No. 6258579
;  GENERAL INFORMATION:
;    APPLICANT:  Mercurio, Frank
;    APPLICANT:  Zhu, Hengyi
;    APPLICANT:  Barbosa, Miguel
;    APPLICANT:  Li, Gian
;    APPLICANT:  Murray, Brion W.
;    TITLE OF INVENTION:  STIMULUS-INDUCIBLE PROTEIN KINASE
;    TITLE OF INVENTION:  COMPLEX AND METHODS OF USE THEREFOR
;    NUMBER OF SEQUENCES:  25
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SEED and BERRY LLP
;      STREET:  6300 Columbia Center, 701 Fifth Avenue
;      CITY:  Seattle
;      STATE:  Washington
;      COUNTRY:  USA
;      ZIP:  98104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/910,820
;      FILING DATE:  12-AUG-1997
;      CLASSIFICATION:  435
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  Maki, David J.
;      REGISTRATION NUMBER:  31,392
;      REFERENCE/DOCKET NUMBER:  860098.413C1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (206) 622-4900
;      TELEFAX:  (206) 682-6031
;  INFORMATION FOR SEQ ID NO:  9:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  756 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:
;      TOPOLOGY:  linear
US-08-910-820-9

  Query Match             100.0%;  Score 151;  DB 3;  Length 756;
  Best Local Similarity   100.0%;  Pred. No. 2.4e-16;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              ||||||||||||||||||||||||||||||
Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


RESULT 12
US-09-109-986-2
; Sequence 2, Application US/09109986
; Patent No. 6479266
;  GENERAL INFORMATION:
;    APPLICANT:  Rothe, Mike
;    APPLICANT:  Cao, Zhaodan
;    APPLICANT:  R gnier, Catherine
;    TITLE OF INVENTION:  IKK-` Proteins, Nucleic Acids and Methods
;    NUMBER OF SEQUENCES:  5
;    CORRESPONDENCE ADDRESS:
;      ADDRESSEE:  SCIENCE & TECHNOLOGY LAW GROUP
;      STREET:  268 BUSH STREET, SUITE 3200
;      CITY:  SAN FRANCISCO
;      STATE:  CALIFORNIA
;      COUNTRY:  USA
;      ZIP:  94104
;    COMPUTER READABLE FORM:
;      MEDIUM TYPE:  Floppy disk
;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/109,986
;      FILING DATE:
;      CLASSIFICATION:
;    PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/890,854
;      FILING DATE:
;    ATTORNEY/AGENT INFORMATION:
;      NAME:  OSMAN, RICHARD A
;      REGISTRATION NUMBER:  36,627
;      REFERENCE/DOCKET NUMBER:  T97-006-1
;    TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (415) 343-4341
;      TELEFAX:  (415) 343-4342
;  INFORMATION FOR SEQ ID NO:  2:
;    SEQUENCE CHARACTERISTICS:
;      LENGTH:  756 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;    MOLECULE TYPE:  peptide
US-09-109-986-2

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RESULT 13
US-09-844-908-9
; Sequence 9, Application US/09844908
; Patent No. 6576437
;  GENERAL INFORMATION:
;       APPLICANT: Mercurio, Frank
;                  Zhu, Hengyi
;                  Barbosa, Miguel
;                  Li, Gian
;                  Murray, Brion W.
;       TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
;                           COMPLEX AND METHODS OF USE THEREFOR
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;            ADDRESSEE: SEED and BERRY LLP
;            STREET: 6300 Columbia Center, 701 Fifth Avenue
;            CITY: Seattle
;            STATE: Washington
;            COUNTRY: USA
;            ZIP: 98104
;       COMPUTER READABLE FORM:
;            MEDIUM TYPE: Floppy disk
;            COMPUTER: IBM PC compatible
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;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/844,908
;             FILING DATE: 27-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/910,820
;             FILING DATE: 12-AUG-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Maki, David J.
;             REGISTRATION NUMBER: 31,392
;             REFERENCE/DOCKET NUMBER: 860098.413C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 622-4900
;             TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 756 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-844-908-9

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RESULT 14
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; Sequence 4, Application US/09868758
; Patent No. 6576439
; GENERAL INFORMATION:
;  APPLICANT: Glaxo Wellcome KK
;  APPLICANT:  Takemoto, Yoshihiro
;  APPLICANT:  Sakai, Yutaka
;  APPLICANT:  Hashimoto, Yasuhiro
;  TITLE OF INVENTION: IKK3
;  FILE REFERENCE: 9950986P
;  CURRENT APPLICATION NUMBER: US/09/868,758
;  CURRENT FILING DATE:  2001-09-27
;  PRIOR APPLICATION NUMBER: GB 9828704.8
;  PRIOR FILING DATE: 1998-12-24
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 756
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-868-758-4

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RESULT 15
US-09-160-483-1
; Sequence 1, Application US/09160483A
; Patent No. 6083732
; GENERAL INFORMATION:
;  APPLICANT: Marcu, Kenneth B.
;  TITLE OF INVENTION: A  BIOLOGICALLY ACTIVE ALTERNATIVE FORM OF THE IKK
;  TITLE OF INVENTION: ALPHA IKB KINASE
;  FILE REFERENCE: Docket No. 6083732: 178-255
;  CURRENT APPLICATION NUMBER: US/09/160,483A
;  CURRENT FILING DATE: 1998-09-25
;  NUMBER OF SEQ ID NOS: 3
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 584
;   TYPE: PRT
;   ORGANISM: mus.musculus domesticus
US-09-160-483-1

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Job time : 19 secs
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GenCore version 5.1.6

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	151	100.0	747	12	US-10-087-192-1755	Sequence 1755, Ap
2	151	100.0	756	9	US-09-796-872-15	Sequence 15, Appl
3	151	100.0	756	9	US-09-771-161A-232	Sequence 232, App
4	151	100.0	756	9	US-09-844-908-9	Sequence 9, Appli
5	151	100.0	756	9	US-09-844-988-9	Sequence 9, Appli
6	151	100.0	756	14	US-10-243-408-2	Sequence 2, Appli
7	151	100.0	756	14	US-10-338-462-9	Sequence 9, Appli
8	151	100.0	756	15	US-10-408-636-4	Sequence 4, Appli
9	151	100.0	756	15	US-10-394-322A-33	Sequence 33, Appl
10	151	100.0	769	12	US-10-087-192-1758	Sequence 1758, Ap
11	79	52.3	745	9	US-09-796-872-2	Sequence 2, Appli
12	79	52.3	745	9	US-09-844-908-10	Sequence 10, Appl
13	79	52.3	745	9	US-09-844-988-10	Sequence 10, Appl
14	79	52.3	745	12	US-10-060-065-14	Sequence 14, Appl
15	79	52.3	745	14	US-10-243-408-4	Sequence 4, Appli
16	79	52.3	745	14	US-10-059-585-35	Sequence 35, Appl
17	79	52.3	745	14	US-10-338-462-10	Sequence 10, Appl
18	79	52.3	745	15	US-10-408-636-3	Sequence 3, Appli
19	79	52.3	745	15	US-10-394-322A-32	Sequence 32, Appl
20	79	52.3	745	16	US-10-741-601-375	Sequence 375, App
21	76	50.3	996	14	US-10-072-036-123	Sequence 123, App
22	76	50.3	997	14	US-10-072-036-121	Sequence 121, App
23	56	37.1	467	12	US-10-282-122A-67939	Sequence 67939, A
24	55	36.4	224	12	US-10-424-599-259148	Sequence 259148,
25	55	36.4	482	12	US-10-424-599-199420	Sequence 199420,
26	54	35.8	383	12	US-10-282-122A-69530	Sequence 69530, A
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28	54	35.8	387	9	US-09-815-242-13750	Sequence 13750, A
29	54	35.8	387	12	US-10-282-122A-56765	Sequence 56765, A
30	54	35.8	387	12	US-10-282-122A-60312	Sequence 60312, A
31	54	35.8	387	12	US-10-282-122A-73063	Sequence 73063, A
32	54	35.8	387	12	US-10-282-122A-75775	Sequence 75775, A
33	54	35.8	387	15	US-10-369-493-23631	Sequence 23631, A
34	54	35.8	388	16	US-10-357-521-15	Sequence 15, Appl
35	54	35.8	391	9	US-09-815-242-5123	Sequence 5123, Ap
36	54	35.8	391	12	US-10-282-122A-43443	Sequence 43443, A
37	54	35.8	391	12	US-10-282-122A-67603	Sequence 67603, A
38	54	35.8	391	15	US-10-447-515-26	Sequence 26, Appl
39	54	35.8	409	15	US-10-369-493-13890	Sequence 13890, A
40	53	35.1	387	12	US-10-282-122A-77565	Sequence 77565, A
41	53	35.1	507	15	US-10-369-493-10701	Sequence 10701, A
42	52	34.4	386	12	US-10-282-122A-56042	Sequence 56042, A
43	52	34.4	387	12	US-10-282-122A-77831	Sequence 77831, A
44	52	34.4	850	15	US-10-369-493-10111	Sequence 10111, A
45	51	33.8	331	16	US-10-437-963-173921	Sequence 173921,

ALIGNMENTS

RESULT 1
US-10-087-192-1755
; Sequence 1755, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
; APPLICANT: Morris, David W.
; APPLICANT: Engelhard, Eric K.
; TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: 529452000122
; CURRENT APPLICATION NUMBER: US/10/087,192
; CURRENT FILING DATE: 2002-03-01
; PRIOR APPLICATION NUMBER: US 09/747,377
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: US 09/798,586
; PRIOR FILING DATE: 2001-03-02
; NUMBER OF SEQ ID NOS: 2059
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1755
; LENGTH: 747
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-087-192-1755

Query Match 100.0%; Score 151; DB 12; Length 747;
Best Local Similarity 100.0%; Pred. No. 1.3e-14;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 2
US-09-796-872-15
; Sequence 15, Application US/09796872
; Patent No. US20020045235A1
; GENERAL INFORMATION:

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;  APPLICANT: Karin, Michael
;  APPLICANT:  DiDonato, Joseph A.
;  APPLICANT:  Rothwarf, David M.
;  APPLICANT:  Hayakawa, Makio
;  APPLICANT:  Zandi, Ebrahim
;  TITLE OF INVENTION: IkB Kinase, Subunits Thereof, and Methods of Using Same
;  FILE REFERENCE: P-UD 3295
;  CURRENT APPLICATION NUMBER: US/09/796,872
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER: 09/168,629
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/061,470
;  PRIOR FILING DATE: 1997-10-09
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15
;   LENGTH: 756
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-796-872-15

  Query Match             100.0%;  Score 151;  DB 9;  Length 756;
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Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


RESULT 3
US-09-771-161A-232
; Sequence 232, Application US/09771161A
; Patent No. US20020110811A1
; GENERAL INFORMATION:
;  APPLICANT: LEVINE, et al.
;  TITLE OF INVENTION: VARIANTS Of PROTEIN KINASES
;  FILE REFERENCE: 802620-2005.1
;  CURRENT APPLICATION NUMBER: US/09/771,161A
;  CURRENT FILING DATE:  2001-01-26
;  PRIOR APPLICATION NUMBER: 09/724,676
;  PRIOR FILING DATE: 2000-11-28
;  PRIOR APPLICATION NUMBER: 136776
;  PRIOR FILING DATE: 2000-06-15
;  PRIOR APPLICATION NUMBER: 135619
;  PRIOR FILING DATE: 2000-04-12
;  NUMBER OF SEQ ID NOS: 273
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;   LENGTH: 756
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;   ORGANISM: Homo sapiens
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RESULT 4
US-09-844-908-9
; Sequence 9, Application US/09844908
; Patent No. US20020151021A1
;   GENERAL INFORMATION:
;        APPLICANT: Mercurio, Frank
;                   Zhu, Hengyi
;                   Barbosa, Miguel
;                   Li, Gian
;                   Murray, Brion W.
;        TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
;                            COMPLEX AND METHODS OF USE THEREFOR
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: SEED and BERRY LLP
;             STREET: 6300 Columbia Center, 701 Fifth Avenue
;             CITY: Seattle
;             STATE: Washington
;             COUNTRY: USA
;             ZIP: 98104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/844,908
;             FILING DATE: 27-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/910,820
;             FILING DATE: 12-AUG-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Maki, David J.
;             REGISTRATION NUMBER: 31,392
;             REFERENCE/DOCKET NUMBER: 860098.413C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 622-4900
;             TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 9:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 756 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-844-908-9

  Query Match             100.0%;  Score 151;  DB 9;  Length 756;
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RESULT 5
US-09-844-988-9
; Sequence 9, Application US/09844988
; Patent No. US20020158764A1
;   GENERAL INFORMATION:
;        APPLICANT: Mercurio, Frank
;                   Zhu, Hengyi
;                   Barbosa, Miguel
;                   Li, Gian
;                   Murray, Brion W.
;        TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
;                            COMPLEX AND METHODS OF USE THEREFOR
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: SEED and BERRY LLP
;             STREET: 6300 Columbia Center, 701 Fifth Avenue
;             CITY: Seattle
;             STATE: Washington
;             COUNTRY: USA
;             ZIP: 98104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
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;             APPLICATION NUMBER: US/09/844,988
;             FILING DATE: 26-Apr-2001
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/910,820
;             FILING DATE: 1997-08-13
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Maki, David J.
;             REGISTRATION NUMBER: 31,392
;             REFERENCE/DOCKET NUMBER: 860098.413C1
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 622-4900
;             TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 756 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-844-988-9

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RESULT 6
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; Sequence 2, Application US/10243408
; Publication No. US20030077683A1
;   GENERAL INFORMATION:
;       APPLICANT: Rothe, Mike
;                  Cao, Zhaodan
;                  R gnier, Catherine
;       TITLE OF INVENTION: IKK-' Proteins, Nucleic Acids and Methods
;       NUMBER OF SEQUENCES: 5
;       CORRESPONDENCE ADDRESS:
;             ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;             STREET: 268 BUSH STREET, SUITE 3200
;             CITY: SAN FRANCISCO
;             STATE: CALIFORNIA
;             COUNTRY: USA
;             ZIP: 94104
;       COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;       CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/243,408
;             FILING DATE: 13-Sep-2002
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/109,986
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/890,854
;             FILING DATE: <Unknown>
;       ATTORNEY/AGENT INFORMATION:
;             NAME: OSMAN, RICHARD A
;             REGISTRATION NUMBER: 36,627
;             REFERENCE/DOCKET NUMBER: T97-006-1
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 343-4341
;             TELEFAX: (415) 343-4342
;   INFORMATION FOR SEQ ID NO: 2:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 756 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;       MOLECULE TYPE: peptide
;       SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-243-408-2

  Query Match             100.0%;  Score 151;  DB 14;  Length 756;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-14;
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Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


RESULT 7
US-10-338-462-9
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; Publication No. US20030100026A1
;   GENERAL INFORMATION:
;       APPLICANT: Mercurio, Frank
;                  Zhu, Hengyi
;                  Barbosa, Miguel
;                  Li, Gian
;                  Murray, Brion W.
;       TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
;                           COMPLEX AND METHODS OF USE THEREFOR
;       NUMBER OF SEQUENCES: 25
;       CORRESPONDENCE ADDRESS:
;             ADDRESSEE: SEED and BERRY LLP
;             STREET: 6300 Columbia Center, 701 Fifth Avenue
;             CITY: Seattle
;             STATE: Washington
;             COUNTRY: USA
;             ZIP: 98104
;       COMPUTER READABLE FORM:
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;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
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;             FILING DATE: 08-Jan-2003
;             CLASSIFICATION: <Unknown>
;       PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/844,908
;             FILING DATE: 27-Apr-2001
;             APPLICATION NUMBER: US/08/910,820
;             FILING DATE: 12-AUG-1997
;       ATTORNEY/AGENT INFORMATION:
;             NAME: Maki, David J.
;             REGISTRATION NUMBER: 31,392
;             REFERENCE/DOCKET NUMBER: 860098.413C1
;       TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 622-4900
;             TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 9:
;       SEQUENCE CHARACTERISTICS:
;             LENGTH: 756 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;       SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-10-338-462-9

  Query Match             100.0%;  Score 151;  DB 14;  Length 756;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

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RESULT 8
US-10-408-636-4
; Sequence 4, Application US/10408636
; Publication No. US20030215879A1
; GENERAL INFORMATION:
;  APPLICANT: Glaxo Wellcome KK
;  APPLICANT:  Takemoto, Yoshihiro
;  APPLICANT:  Sakai, Yutaka
;  APPLICANT:  Hashimoto, Yasuhiro
;  TITLE OF INVENTION: IKK3 Kinase
;  FILE REFERENCE: PJ3630US2
;  CURRENT APPLICATION NUMBER: US/10/408,636
;  CURRENT FILING DATE:  2003-04-07
;  PRIOR APPLICATION NUMBER: GB 9828704.8
;  PRIOR FILING DATE: 1998-12-24
;  NUMBER OF SEQ ID NOS: 45
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
;   LENGTH: 756
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-408-636-4

  Query Match             100.0%;  Score 151;  DB 15;  Length 756;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
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Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


RESULT 9
US-10-394-322A-33
; Sequence 33, Application US/10394322A
; Publication No. US20030232391A1
; GENERAL INFORMATION:
;  APPLICANT: SUNESIS PHARMACEUTICALS, INC.
;  APPLICANT:  Prescott, John C.
;  TITLE OF INVENTION: IDENTIFICATION OF KINASE INHIBITORS
;  FILE REFERENCE: 39750-0006 US
;  CURRENT APPLICATION NUMBER: US/10/394,322A
;  CURRENT FILING DATE:  2003-03-20
;  PRIOR APPLICATION NUMBER: US 60/366,892
;  PRIOR FILING DATE: 2002-03-21
;  NUMBER OF SEQ ID NOS: 70
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 33
;   LENGTH: 756
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-394-322A-33

  Query Match             100.0%;  Score 151;  DB 15;  Length 756;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
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Db        535 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 564


RESULT 10
US-10-087-192-1758
; Sequence 1758, Application US/10087192
; Publication No. US20020182586A1
; GENERAL INFORMATION:
;  APPLICANT: Morris, David W.
;  APPLICANT:  Engelhard, Eric K.
;  TITLE OF INVENTION: NOVEL COMPOSITIONS AND METHODS FOR
;  TITLE OF INVENTION:  CANCER
;  FILE REFERENCE: 529452000122
;  CURRENT APPLICATION NUMBER: US/10/087,192
;  CURRENT FILING DATE:  2002-03-01
;  PRIOR APPLICATION NUMBER: US 09/747,377
;  PRIOR FILING DATE: 2000-12-22
;  PRIOR APPLICATION NUMBER: US 09/798,586
;  PRIOR FILING DATE: 2001-03-02
;  NUMBER OF SEQ ID NOS: 2059
;  SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1758
;   LENGTH: 769
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-087-192-1758

  Query Match             100.0%;  Score 151;  DB 12;  Length 769;
  Best Local Similarity   100.0%;  Pred. No. 1.3e-14;
  Matches   30;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
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Db        548 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 577


RESULT 11
US-09-796-872-2
; Sequence 2, Application US/09796872
; Patent No. US20020045235A1
; GENERAL INFORMATION:
;  APPLICANT: Karin, Michael
;  APPLICANT:  DiDonato, Joseph A.
;  APPLICANT:  Rothwarf, David M.
;  APPLICANT:  Hayakawa, Makio
;  APPLICANT:  Zandi, Ebrahim
;  TITLE OF INVENTION: IkB Kinase, Subunits Thereof, and Methods of Using Same
;  FILE REFERENCE: P-UD 3295
;  CURRENT APPLICATION NUMBER: US/09/796,872
;  CURRENT FILING DATE:  2001-02-28
;  PRIOR APPLICATION NUMBER: 09/168,629
;  PRIOR FILING DATE: 1998-10-08
;  PRIOR APPLICATION NUMBER: 60/061,470
;  PRIOR FILING DATE: 1997-10-09
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 745
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-796-872-2

  Query Match             52.3%;  Score 79;  DB 9;  Length 745;
  Best Local Similarity   43.3%;  Pred. No. 0.0023;
  Matches   13;  Conservative   11;  Mismatches    6;  Indels    0;  Gaps    0;

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Db        532 DQIMSLHAEIMELQKSPYGRRQGDLMESLE 561


RESULT 12
US-09-844-908-10
; Sequence 10, Application US/09844908
; Patent No. US20020151021A1
;   GENERAL INFORMATION:
;        APPLICANT: Mercurio, Frank
;                   Zhu, Hengyi
;                   Barbosa, Miguel
;                   Li, Gian
;                   Murray, Brion W.
;        TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
;                            COMPLEX AND METHODS OF USE THEREFOR
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: SEED and BERRY LLP
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;             STREET: 6300 Columbia Center, 701 Fifth Avenue
;             CITY: Seattle
;             STATE: Washington
;             COUNTRY: USA
;             ZIP: 98104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/844,908
;             FILING DATE: 27-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/08/910,820
;             FILING DATE: 12-AUG-1997
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Maki, David J.
;             REGISTRATION NUMBER: 31,392
;             REFERENCE/DOCKET NUMBER: 860098.413C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 622-4900
;             TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 745 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-844-908-10

  Query Match             52.3%;  Score 79;  DB 9;  Length 745;
  Best Local Similarity   43.3%;  Pred. No. 0.0023;
  Matches   13;  Conservative   11;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              :::|:|  :|::||:|| ||:||  :: ||
Db        532 DQIMSLHAEIMELQKSPYGRRQGDLMESLE 561


RESULT 13
US-09-844-988-10
; Sequence 10, Application US/09844988
; Patent No. US20020158764A1
;   GENERAL INFORMATION:
;        APPLICANT: Mercurio, Frank
;                   Zhu, Hengyi
;                   Barbosa, Miguel
;                   Li, Gian
;                   Murray, Brion W.
;        TITLE OF INVENTION: STIMULUS-INDUCIBLE PROTEIN KINASE
;                            COMPLEX AND METHODS OF USE THEREFOR
;        NUMBER OF SEQUENCES: 25
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: SEED and BERRY LLP
;             STREET: 6300 Columbia Center, 701 Fifth Avenue
;             CITY: Seattle
;             STATE: Washington
;             COUNTRY: USA
;             ZIP: 98104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/09/844,988
;             FILING DATE: 26-Apr-2001
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: 08/910,820
;             FILING DATE: 1997-08-13
;        ATTORNEY/AGENT INFORMATION:
;             NAME: Maki, David J.
;             REGISTRATION NUMBER: 31,392
;             REFERENCE/DOCKET NUMBER: 860098.413C1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (206) 622-4900
;             TELEFAX: (206) 682-6031
;   INFORMATION FOR SEQ ID NO: 10:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 745 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: <Unknown>
;             TOPOLOGY: linear
;        SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-844-988-10

  Query Match             52.3%;  Score 79;  DB 9;  Length 745;
  Best Local Similarity   43.3%;  Pred. No. 0.0023;
  Matches   13;  Conservative   11;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 ERMMALQTDIVDLQRSPMGRKQGGTLDDLE 30
              :::|:|  :|::||:|| ||:||  :: ||
Db        532 DQIMSLHAEIMELQKSPYGRRQGDLMESLE 561


RESULT 14
US-10-060-065-14
; Sequence 14, Application US/10060065
; Publication No. US20030017480A1
; GENERAL INFORMATION:
;  APPLICANT: Toshio Ota
;  APPLICANT:  Takao Isogai
;  APPLICANT:  Tetsuo Nishikawa
;  APPLICANT:  Koji Hayashi
;  APPLICANT:  Kaoru Otsuka
;  APPLICANT:  Jun-Ichi Yamamoto
;  APPLICANT:  Shizuko Ishii
;  APPLICANT:  Tomoyasu Sugiyama
;  APPLICANT:  Ai Wakamatsu
;  APPLICANT:  Keiichi Nagai
;  APPLICANT:  Tetsuji Otsuki
;  APPLICANT:  Shin-Ichi Funahashi
;  APPLICANT:  Chiaki Senoo
;  APPLICANT:  Jun-Ichi Nezu
;  TITLE OF INVENTION: NOVEL GENES ENCODING PROTEIN KINASE/PROTEIN PHOSPHATASE
;  FILE REFERENCE: 06501-099002
;  CURRENT APPLICATION NUMBER: US/10/060,065
;  CURRENT FILING DATE:  2002-01-29
;  PRIOR APPLICATION NUMBER: PCT/JP00/05061
;  PRIOR FILING DATE: 2000-07-28
;  PRIOR APPLICATION NUMBER: US 60/159,590
;  PRIOR FILING DATE: 1999-10-18
;  PRIOR APPLICATION NUMBER: US 60/183,322
;  PRIOR FILING DATE: 2000-02-17
;  PRIOR APPLICATION NUMBER: JP 11-248036
;  PRIOR FILING DATE: 1999-07-29
;  PRIOR APPLICATION NUMBER: JP 2000-118776
;  PRIOR FILING DATE: 2000-01-11
;  PRIOR APPLICATION NUMBER: JP 2000-183767
;  PRIOR FILING DATE: 2000-05-02
;  PRIOR APPLICATION NUMBER: JP 2000-241899
;  PRIOR FILING DATE: 2000-06-09
;  NUMBER OF SEQ ID NOS: 43
;  SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
;   LENGTH: 745
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-060-065-14

  Query Match             52.3%;  Score 79;  DB 12;  Length 745;
  Best Local Similarity   43.3%;  Pred. No. 0.0023;
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  Matches   13;  Conservative   11;  Mismatches    6;  Indels    0;  Gaps    0;

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              :::|:|  :|::||:|| ||:||  :: ||
Db        532 DQIMSLHAEIMELQKSPYGRRQGDLMESLE 561


RESULT 15
US-10-243-408-4
; Sequence 4, Application US/10243408
; Publication No. US20030077683A1
;   GENERAL INFORMATION:
;        APPLICANT: Rothe, Mike
;                   Cao, Zhaodan
;                   R gnier, Catherine
;        TITLE OF INVENTION: IKK-' Proteins, Nucleic Acids and Methods
;        NUMBER OF SEQUENCES: 5
;        CORRESPONDENCE ADDRESS:
;             ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
;             STREET: 268 BUSH STREET, SUITE 3200
;             CITY: SAN FRANCISCO
;             STATE: CALIFORNIA
;             COUNTRY: USA
;             ZIP: 94104
;        COMPUTER READABLE FORM:
;             MEDIUM TYPE: Floppy disk
;             COMPUTER: IBM PC compatible
;             OPERATING SYSTEM: PC-DOS/MS-DOS
;             SOFTWARE: PatentIn Release #1.0, Version #1.30
;        CURRENT APPLICATION DATA:
;             APPLICATION NUMBER: US/10/243,408
;             FILING DATE: 13-Sep-2002
;             CLASSIFICATION: <Unknown>
;        PRIOR APPLICATION DATA:
;             APPLICATION NUMBER: US/09/109,986
;             FILING DATE: <Unknown>
;             APPLICATION NUMBER: 08/890,854
;             FILING DATE: <Unknown>
;        ATTORNEY/AGENT INFORMATION:
;             NAME: OSMAN, RICHARD A
;             REGISTRATION NUMBER: 36,627
;             REFERENCE/DOCKET NUMBER: T97-006-1
;        TELECOMMUNICATION INFORMATION:
;             TELEPHONE: (415) 343-4341
;             TELEFAX: (415) 343-4342
;   INFORMATION FOR SEQ ID NO: 4:
;        SEQUENCE CHARACTERISTICS:
;             LENGTH: 745 amino acids
;             TYPE: amino acid
;             STRANDEDNESS: single
;             TOPOLOGY: linear
;        MOLECULE TYPE: peptide
;        SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-243-408-4

  Query Match             52.3%;  Score 79;  DB 14;  Length 745;
  Best Local Similarity   43.3%;  Pred. No. 0.0023;
  Matches   13;  Conservative   11;  Mismatches    6;  Indels    0;  Gaps    0;

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